

#### STIC Database Tracking Number: 137736

TO: Bao-Qun Li

Location: rem/3d24/3c18

Art Unit: 1648

Wednesday, November 17, 2004 Case Serial Number: 10/784537 From: Paul Schulwitz

**Location: Biotech-Chem Library** 

**REM-1A65** 

Phone: (571)272-2527

paul.schulwitz@uspto.gov

#### Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527



Aar19363 homo

Q9vsk1 drosophila Q96js2 homo sapien Q96js2 homo sapien Q90827 gallus gall Q9fkn3 arabidopsis P98092 bombyx mori Q8axc3 xenopus lae P22652 gallid herp P22653 gallid herp Q77mr7 meleagrid h Aaf66780 turkey he Aag14238 turkey he Aag14238 turkey he

Scoring table:

Searched:

Minimum DB Maximum DB M

Database

Result Š.

Perfect score:

Sequence:

OM protein

Run on:

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MEDLINE-21595285; PubMed=11759840;

MEDLINE-21595285; PubMed=11759840;

MEDLINE-21595285; PubMed=11759840;

MEDLINE-21595285; PubMed=11759840;

Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Makazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213 (2001).

REMBL; APRO03589; BAB14007.1; -.

R GO; GO:0005189; Feiectron transporter activity; IEA.

GO; GO:0005189; Peiectron transport; IEA.

R GO; GO:000518; Peiectron transport; IEA.

R PRINTS; PRO037; Fer4; 1..

R PROSTIE; PRO037; Fer4; 1..

R PROSTIE; PRO0359; FER4S FERENDXIN.

R PROSTIE; PRO0359; FER4S FERENDXIN.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PMM1560;
Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4Pe-45; Complete protecome; Iron; Iron-sulfur; Metal-binding SEQUENCE 425 AA; 46348 MW; 7237DCE3EFD6912E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 425;
                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Last annotation update)
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Pred. No. 12;
0; Mismatches
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          Q9VSK1
Q96JS2
NEL2 HUMAN
NEL_CHICK
                                                                    HMCT BOMMO
QBAXC3
UL45 GAHVB
                                                                                                       UL45 GAHVM
Q77MR7
AAF66780
AAG14238
AAS01688
 AAR19363
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77.8%;
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                                                                                                                                                                                                                                                                                                           Alr2308 protein.
OrderedLocusNames=alr2308;
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Matches 7; Conservative
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SEQUENCE
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06ikm6 drosophila
082243 martek's dis
078299 gallid herp
078224 homo sapien
020000 caenorhabdi
07rdg plasmodium
07rdg synechocyst
06uxg homo sapien
Aag88617 homo sapien
Aag88617 homo sapien
055456 synechocyst
08269 streptomyce
06g1k1 staphylococ
06g1k1 staphylococ
06g1k1 staphylococ
099w00 staphylococ
07a7d2 staphylococ
07a64 mycobacteri
07mm5 vibrio para
08d6n3 vibrio vuln
07d460 anopheles g
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Q7uzu5 prochloroco
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                                                                                 November 16, 2004, 14:14:16; Search time 53.6604 Seconds (without alignments) 96.503 Million cell updates/sec
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Q6s518
Q8iyw3
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                           protein search, using sw model
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0704K2
020000
020000
07MBG7
07MBG7
07WH5
06UXQ3
06UXQ3
06GC16
08CXX1
08NY13
09SZZ0
09SZZ0
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Q7UZU5
Q8GL14
Q6IKM6
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Gapop 10.0 , Gapext 0.5
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38HXE2
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2: uniprot_trembl:*
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seq length: 2000000000
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Match Length
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Gaps

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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;

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PRELIMINARY;
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74 PRQCDSIC 81
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05-JUL-2004
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                                                                         STRAIN=PCC 7942;

MEDLINE=22450571; PubMed=12562813;

Matayama M., Kondo T., Xiong J., Golden S.S.;

**IdpA encodes an irror-sulfur protein involved in light-dependent modulation of the circadian period in the cyanobacterium Synechococcus elongatus PCC 7942.";

J. Bacteriol. 185:1415-1422 (2003).

EMBL, AY136759; AAN06910.1; -.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0005618; P:electron transporter iEA.

GO; GO:0005018; P:electron transport. IEA.

GO; GO:0005018; P:electron binding; IEA.

GO; GO:0005018; P:electron binding; IEA.

Fam: Pro0017; Ferts, IEA.

Fam: Pro0017; Ferts, IEA.
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66.7%; Pred. No. 21;
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PROSTIE; PS00198; 4FE4SF FERREDOXIN; 1.
4FE-4S; Iron-sulfur; Metal-binding.
SEQUENCE 352 AA; 37865 MW; 33614612158F2936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 AA; 37282 MW; CBC53CA6F8A27AB3 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                         NCBI_TaxID=59919;
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-! MISCELLANBOUS: The sequence shown here is derived from an EMBL/Genbank/DDBJ third party annotation (TPA) entry.

EMBL, BK002340; DAA03846.1; ...
SEQUENCE 146 AA; 15612 MW; D23DCA44DCFAABC5 CRC64;
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                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Jang H., Cai J., Izumiya Y., Murakami Y., Mochizuki M., Song
Lee Y., Kai C., Takahashi E., Mikami T.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB012572; BAA32581.1; -.
EMBL; AB024414; BAA82941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.7%; Score 42; DB 2; Length 146; 75.0%; Pred. No. 29;
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Interpro; IPR009817; Varicello_UL45.
Pfam; PF07144; Varicello_UL45; 1.
SEQUENCE 210 AA; 2303@ NW; 6ED41E888FC10E53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marek's disease virus serotype 2 MDV2.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
NCBI_TaxID=36353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Virion protein (UL45 product homolog).
Name-UL45; Synonyms-ORF 53;
                        05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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(TrEMBLrel. 27,
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Score 42; DB 2;
Pred. No. 65;
2; Mismatches 2
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
           73.7%;
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Query Match
Best Local Similarity 55.6
----- 5; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                                             Name=HN1; Synonyms=HN1A;
Homo sapiens (Human).
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152 CPERCRSVC 160
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Leimbach D.;
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X MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
A Palenik B., Barhamsha B., Larimer F.W., Land M.L., Hauser L.,
A Chain P., Lamerdin J.E., Regala W., Allen B.E., McCarren J.,
A Pauleni T.T., Duffresne A., Partensky F., Webb E.A., Waterbury J.;
The genome of a motile marine Synechococcus.";
I Nature 4424.1377-1042(2003).
R EMBL; BX569694; CAE08580.1; -
R GO; GO:0005489; F:electron transporter activity; IEA.
R GO; GO:0005189; F:electron transport; IEA.
R GO; GO:000518; P:electron transport; IEA.
R InterPro; IPR00450; 4Fe45_ferredoxin.
R PROSITE; PS001098; 4Fe45_ferredoxin.
R PROSITE; PS001098; 4Fe45_FERREDOXIN; ITAL.
                                    Gaps
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"A Complete Genomic DNA Sequence of Marek's Disease Virus Type 2,
Strain HPRS24.";
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         Score 42; DB 2; Length 210;
Pred. No. 41;
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Pred. No. 41;
1; Mismatches 2; Indels
                                    2; Indels
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EMBL, AB049735; BAB1655.1; -.

InterPro; IPR009817; Varicello_UL45.

Pfam; PF07144; Varicello_UL45; 1.

SEQUENCE 210 AA; 23038 MW; 6ED41E888FC10E53 CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                            Gallid herpesvirus 3.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
                                                                                                                                                                                Last sequence update)
Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                  1; Mismatches
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           73.78;
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Best Local Similarity 66.7
Matches 6; Conservative
                                  6; Conservative
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                                                                         161 CPRTCTAIC 169
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           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                NCBI_TaxID=35250;
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Q7U4K2;
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05-UTL-2004 (TREMBLRel. 27, Last annoctation update)
Hematological and neurological expressed protein 1B (Hematological and neurological expressed protein b).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-UNV-1996 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein P35A5.4.
CRENames=P35A5.4;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.9%; Score 41; DB 2; Length 181; 55.6%; Pred. No. 52;
                                                              Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; A7322169; AAPB3381.; -.
EMBL; A7348672; AAPB33962.1; -.
SEQUENCE 181 AA; 19916 MW; FF644A114DE28850 CRC64;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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strain 1.
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                                                  RESULT 11
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Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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preliminary data.

EMBL; AABLO1001731; EAA17486.1; -.

GO; GO:00003870; F:5-aminolevulinate synthase activity; IEA.

GO; GO:0000583; F:transaminase activity; IEA.

GO; GO:0006783; P:heme biosynthesis; IEA.

R InterPro; IPR001961; Saminolev synth.

R InterPro; IPR001989; Aminotrans I/I.

R InterPro; IPR001917; Aminotrans I/II.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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Pred. No. 76;
4; Mismatches 1; Indels
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55.6%; Pred. No. 1.7e+02;
ive 3; Mismatches 1; Indels
Waterston R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, U46675, AAB52645.1; -.
PIR; T16246; T16246.
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Pfam; PF00155; Aminorran 1 2; 1.
TIGRPAM; TIGRO1821; Saminolev synth; 1.
PROSITE; PRO0599; AA TRANSFER CLASS 2; UNKNOWN 1.
SEQUENCE 631 AA; 72951 MW; D266EDB7255CD842 CRC64;
                                                                                        WormPep; F35A5.4; CE04488.
InterPro; IPR003341; DUF139.
Pfam; PF02363; C_tripleX; 9.
Hypothetical protein:
SEQUENCE 273 AA; 29231 MW; 11542812CC566530 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-21004 (TrEMBLrel. 26, Last annotation update)
Delta-aminolevulinic acid synthetase.
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Best Local Similarity 44.**,
4; Conservative
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les 5; Conservative
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MEDLINE=22882897; PubMed=14500908;

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MEDLINE=22882897; PubMed=14500908;

MEDLINE=22882897; PubMed=14500908;

MEDLINE=22882897; PubMed=14500908;

Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

Meyer F., Lederer H., Schuster S.C.;

Meyer F., Lisulfide oxidoreductase activity; IEA.

Meyer F., Lederer H., Schuster S.C.;

Meyer F., Rederer H., Schuster S.C.;

Meyer F., Rederer H., Schuster S.C.;

Meyer F., Rederer H., Schuster S.C.;

Meyer F., Rederer
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                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Wolinella.
NCBI_TaxID=844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATEDEHYDROGENASE (EC
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Last annotation update)
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EMBL; BX294137; CAD72749.1; -.
InterPro; IPR004619; Baf.
649 AA
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Name=FDHB; OrderedLocusNames=WS0477;
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SEQUENCE 649 AA; 72557 MW; CCA
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
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PRELIMINARY;
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055456
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Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
Chow B., Choui C., Crowley C., Currell B., Deuel B., Dowd P.,
Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                 Score 40, DB 2; Length 295;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
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TIGRFAMs; TIGR00671; baf; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 295 AA; 31445 MW; 430B95673709B7A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42782 MW; 558D4E2167B69AF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bioinformatics assessment.";
Genome Res. 13:255-227(012003).
EMBL; AY358250; AAQ88617.1; -.
InterPro; IPR0011036; PH related.
InterPro; IPR006019; PID domain.
InterPro; IPR006020; PTB PID.
                                                                                     70.2%;
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PRINTS; PR00629; SHCPIDOMAIN.
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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PROSITE; PS01179; PID; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 387 AA; 42782
                                                                                                       Best Local Similarity 85.7
Matches 6; Conservative
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Pfam; PF00017; SH2; 1.
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89 RECESVC 95
                                                                                                                                                                        3 RECESIC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=UNQ6438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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AAQ88617;
02-MAR-2004 (
02-MAR-2004 (
02-MAR-2004 (
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Q6UXQ3
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Clark H.F., Gurney A.L., Abaya E., Currell B., Deuel B., Dowd P., Chen J., Chow B., Chul C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Roster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6603. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2.153-166(1995).
EMBL; D64006; BAA10799.1; -.
PIR; 875952.
HSSP; P00193; 1DUR.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.2%; Score 40; DB 2; Length 387; 55.6%; Pred. No. 1.5e+02; ative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bioinformatics Assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; AX358250; AAQ88617.1; -.
SEQUENCE 387 AA; 42782 MW; 558D4E2167B69AF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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MEDLINE=97061201; PubMed=8905231;
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OrderedLocusNames=sl10031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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Homo sapiens (Human)
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Best Local Similarity
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                                                                                                     NCBI_TaxID=9606;
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DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR001450; 4Fe45_ferredoxin.

DR Pfam; PF00037; FF44; 1.

DR PRINTS; PR00353; 4F45ERRDOXIN.

DR PROSITE; PS00198; 4FE45_FRDOXIN.

NW 4Fe-45; Complete proteome; Iron; Iron-sulfur; Metal-binding.

SQ SEQUENCE 395 AA; 43410 MW; 077421437A6B0DC0 CRC64;

Query Match

Query Match

A0.24; Scoed, DB 2; Length 395;

Best Local Similarity 55.64; Pred. No. 1.6+102;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Search completed: November 16, 2004, 14:29:46 Job time : 55.6604 secs

1 CPRECESIC 9 |||| :| 131 CPRPCAQVC 139

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; Search time 74.0755 Seconds (without alignments) 62.956 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries A Geneseq 23Sep04:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp19908:\* geneseqp2000s:\* geneseqp20018:\* ..... Database

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1	•	Abd60448 Selective	Abr56860 Aminopept	Aaw13427 Breast tu	Aaw60290 Breast ca	Aaw93627 Breast tu	Aab17959 Integrin-	Aab17923 VEGF anta	Aab21702 Human bre	Aae06280 Human bre	Aau81104 Integrin-		Inte	_	Adj51706 CH1 delet	Abg66755 Human nov	Abg66701 Human nov	_	Adi23265 Human MUC	Adj92337 Mouse hai	Aab39289 Gene 38 h	Aay65429 Human 5'	Aam95477 Human rep
SUMMARIES	ABG60452	ABR56864	ABG60448	ABR56860	AAW13427	AAW60290	AAW93627	AAB17959	AAB17923	AAB21702	AAE06280	AAU81104	ABB72956	ADJ73110	ADJ52745	ADJ51706	ABG66755	ABG66701	ADJ69349	ADL23265	ADJ92337	AAB39289	AAY65429	AAM95477
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Length	13	13	9 67	6	13	13	13	13	13	13	13	13	13	13	13	13	1364	1364	1594	5703	177	64	98	121
% Query Match	100.0	100.0	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	58.3	57.1	57.1	57.1
Score	84	2 2	202	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	49	48	48	48
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ABB96162 ABP69453 ABB69453 ABB69837 ABR41785 ABG60450 AABG6124 ABU24727 ABU24727 ABBC2331 AAO21297 AAO21297 AAR31199 ABR431176 AAR80633	ABB69268 AAE18207 ADD18192 AAC27065 AAY06816
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## ALIGNMENTS

Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; aradiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic; ABG60452 standard; peptide; 13 AA. Selective targeting peptide #127. (first entry) gene therapy. 30-JUL-2002 ABG60452; 

07-SEP-2001; 2001WO-US027692. WO200220769-A1 14-MAR-2002. Synthetic.

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.

(TEXA ) UNIV TEXAS SYSTEM. Pasqualini R;

Arap W,

WPI; 2002-415731/44.

Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular disease.

Claim 22; Page 109; 317pp; English.

The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, archritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with ischaemia, cancer, arthritis, diabetes, cardiovascular disease.

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Indels

Length 13;

100.0%; Score 84; DB 6; L 100.0%; Pred. No. 0.00011; iive 0; Mismatches 0;

Local Similarity 100.

Query Match Best Loc Matches

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The present invention describes a method for treating obesity or a lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and (d) inducing weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teracogenic activity. ABRS6806 to ABRS6827, and ACC79106 to ACC79111 represent sequences used in the
           for diagnosing the diseases citted above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60326-ABG60574 represent selective targeting peptides of the invention
inflammation or macular degeneration. Furthermore, the peptide is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic;
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                ö
                                                                                                                                                                        100.0%; Score 84; DB 5; Length 13; 100.0%; Pred. No. 0.00011;
                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aminopeptidase A (APA) binding peptide SEQ ID NO:60.
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Page 104; 247pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kolonin MG;
                                                                                                                                                                                                                                                                                                                                                                                      ABR56864 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2002; 2002WO-US027836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001; 2001WO-US027692
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                       1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                   1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasqualini R, Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-371749/35.
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003022991-A2
                                                                                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                            ABR56864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subject.
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                888888888
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Bacteroides fragilis.

WO200277183-A2.

03-OCT-2002.

Protein encoded by Prokaryotic essential gene #6420.

(first entry)

19-JUN-2003

ABU20893;

ABU20893 standard; protein; 762 AA

ABU20893

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요

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Wang L, Wall D,

WPI; 2003-029926/02 N-PSDB; ACA24763

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.

21-MAR-2001; 2001US-00815242.

08-FEB-2002; 2002US-00072851.

(BLIT-) ELITRA PHARM INC. Zamudio C, Trawick JD,

21-MAR-2002; 2002WO-US009107.

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid concluded are: (2) a host cell containing the vector; (3) an isolated concluded or its fragment whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of against a biological pathway in colliferation or the activity of against a biological pathway or required for proliferation, (7) identifying a compound that inhibits cellular proliferation; (8) identifying a gene product or that has an activity against a biological pathway or required for proliferation, or that inhibits cellular proliferation of an identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibicitic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibicitic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the culture complement or collection of strains; or (13) identifying the target of a compound that inhibits the culture complement or collection of strains; or (13) identifying the target of a compound that inhibits the captured for cultured concludes are useful for identifying proteins or screening for homologous nucleic acids are useful for cellular proliferation to isolate can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 48817; 1766pp; English.
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exemplification of the present invention

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Sequence 13

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drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at from part of the printed secuences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; acardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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7
                                                                                                                                                                                                                                                                                                                                     Length 762;
                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                 DB 6;
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                            Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Page 102; 317pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG60448 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selective targeting peptide #123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000US-0231266P.
17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001; 2001WO-US027692
                                                                                                                                                                                                                                                                                                                                        60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGRVCPQEKQCESKC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CPKVCPRE--CESNC 13
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0.
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                          Sequence 762 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease.
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XX ABG6

XX ABG7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to a
                                                                                                                                                                                                                                                                                                                                                            Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for treating obesity or a
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                              Score 50; DB 5; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
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                                                                                                                                                                                                                                                                                                                              Aminopeptidase A (APA) binding peptide SEQ ID NO:56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 6; 1
Pred. No. 1.7e+06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention
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                                                                                                                                                                                                                           ABR56860 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arap W, Kolonin
                                59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2002; 2002WO-US027836
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                                                                                                                                                                                                                                                                                            (first entry)
                                                                  8; Conservative
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                                                                                                    5 CPRECESNC 13
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                                                                                                                                      CPRECESIC
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Best Local Similarity
Matches 8; Conserv
                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003022991-A2
Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                              Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                             ABR56860;
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13

5 CPRECESNO

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RESULT

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Tumour homing molecules and their conjugates - useful for, e g. directing linked moiety to tumour containing angiogenic vasculature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present peptide represents a tumour homing peptide, and is produced by in vivo panning. The peptide homes to a breat carcinoma. The in vivo panning comprises administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying a peptide that homes to the tumour, collecting a sample of normal tissue corresponding to the tumour, and determining that the peptide that homes to the tumour is not present in the normal lissue. The tumour homins peptide can be linked to a moiety (e.g. doxorubicin), and used to direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour homing peptide; tumour; diagnosis; endothelial cell; breast; andiogenic vasulature; anti-tumour; anti-inflammatory; anti-angiogenic; anti-arthritic; NGR receptor; inhibitor; angiogenesis; anticancer drug; prognosis; inflammation; regeneration; wounded tissue; targetting; macular degeneration; diabetic retinopathy; rheumatoid arthritis;
Tumour homing peptide; in vivo panning; breast carcinoma;
alpha-V-containing integrin binding motif; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.5%; Score 50; DB 2
53.8%; Pred. No. 3.8;
:ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 6; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW93627 standard; protein; 13 AA.
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98US-00139802
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                            Pasqualini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the moiety to a tumour
                                                                                                                                                                                                                                                                 (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                               WPI; 1998-207151/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         occlusive thrombus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                                                         Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09913329-A1
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25-AUG-1998;
                                                                                                                                                                                 10-SEP-1997;
                                                                                                                                                                                                                           10-SEP-1996;
                                                             Unidentified
                                                                                                   WO9810795-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1999
                                                                                                                                           19-MAR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This synthetic peptide is a claimed example of a breast tumour-homing peptide that was identified using a novel method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method typically involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vacular tissue or tumour tissue. The isolated peptides (see AAW13412-52, AAW1181-86) can be used to target e.g. drugs, toxins or labble to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they maintain specificity in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obtaining compound that homes to selected organ or tissue - by in vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                   cancer; in vivo panning; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 50; DB 2; Length 13; 53.8%; Pred. No. 3.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast carcinoma tumour homing peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW60290 standard; peptide; 13 AA.
                                                                                               AAW13427 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 68; 75pp; English
                                                                                                                                                                                                                                                               Breast tumour homing peptide; phage display; drug delivery.
                                                                                                                                                                                                                         Breast tumour homing peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US014600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00526710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00526708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasqualini R;
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CGRECPRLCQSSC 13
                                                                                                                                                                                 (first entry)
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Matches 7; Conservative
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CPRECESIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                     WO9710507-A1
                                                                                                                                                                                 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1997
                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                         AAW13427;
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RESULT 7
AAW60290
ID AAW6
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AC AAW6
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                                                                                                                                                                        vasculature, specifically of a tumour and which have anti-tumour, anti-
inflammatory, anti-angiogenic and anti-arthritic activity. Such molecules
are identified by treating a purified NGR receptor with a test compound
and identifying compounds that bind specifically to the NGR receptor. The
peptides of the invention are inhibitors of angiogenesis and can be used
to produce conjugates for delivering agents to angiogenic vasculature,
particularly anticancer drugs or an imaging agent, for diagnosis or
prognosis. These conjugates may be directed to non-tumour angiogenic
to prognosis. These conjugates may be directed to non-tumour angiogenic
corrections. The present in inflammatory, regenerating or wounded
tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
or rheumatoid arthritis. The peptides provide specific targeting to
theorem to arthritis. The peptides provide specific targeting to
the seposed to the circulation only in angiogenic vasculature. Precise
targeting should reduce the systemic toxicity of anticancer drugs in the
conjugates. Complete killing of all target cells may not be essential
since partial denudation of endothelium may result in an occlusive
thrombus, and endothelial cells are unlikely to become resistant to
anticancer agents nor to lose the targeting receptor. AAM93622-W93809 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                            that home to angiogenic vasculature used as targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAW93843-44 are examples of tumour homing peptides used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                              This invention describes novel peptides which home to angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 50; DB 2; Length 13; 53.8%; Pred. No. 3.8; 1ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Integrin-binding peptide sequence SEQ ID NO:1071.
                                                                                                                                     Example II; Page 67; 180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17959 standard; peptide; 13 AA.
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                                     Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPKVCPRECESNC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.8
Matches 7; Conservative
                                                                                            Identifying molecules
                                                                                                          for anticancer agents.
              (BURN-) BURNHAM INST
                                                                  WPI; 1999-215158/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40200024782-A2
                                       Ruoslahti E,
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22-OCT-1999;
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
confidently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
(L2)d-P2-(L3)e-P3, or -(L1)c-P1, -(L3)c-P3-(L4)f-P4 where P1, P2,
C1 (L2)d-P2-(L3)e-P3, or -(L1)c-P1, -(L3)d-P3-(L4)f-P4 where P1, P2,
C2 (L2)d-P2-(L3)e-P3, or -(L1)c-P1, -(L2)d-P2-(L3)f-P3-(L4)f-P4 where P1, P2,
C3 and P4 = are each independently sequences of pharmacologically active
C3 and b is 1. The composition can have cytostatic, antiasthmatic,
C4 c and b is 1. The composition can have cytostatic, antiasthmatic,
C5 d and b is 1. The composition can have cytostatic, antiasthmatic,
C6 and b is 1. The composition can be used for producing pharmaceutical
C6 compositions. The compositions are useful for treating cancer, asthma,
C7 thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
C7 a Fab domain) can provide a longer half-life or incorporate functions
C8 cuch as Pc receptor binding, protein A binding, complement fixation, and
C7 AAB18013 represent nucleotide and amino acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TFO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
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Pred. No. 3.8;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF antagonist peptide sequence SEQ ID NO:1027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
                                                                Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                                                                                                                                                                                                                                                                                               Claim 39; Page 589; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17923 standard; peptide; 13 AA.
                                                            Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US025044.
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Best Local Similarity 53...
7; Conservative
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                                                                                                                                WPI; 2000-350702/30
(AMGE-) AMGEN INC.
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                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 AA;
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22-OCT-1999;
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                                                                Feige U,
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Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 90; 118pp; English.
                                                                                                                                                                                                                                                                                                                            WPI; 2000-499174/44.
                                                                                                                                   Sequence 13 AA;
                                                                                                                                                                                                                                                                  WO200042973-A2
                                                                                                                                                                                                                                                                                               22-JAN-1999;
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                             27-JUL-2000.
                                                                                                                                                                                                             AAB21702;
                                                                                                                                             Query Match
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AAB21702
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The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is human breast tumour homing peptide. This sequence is useful in the homing of pro-apoptotic conjugates of the invention The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is a homing peptide isolated in the present invention, which can be conjugated to an antimicrobial peptide to make the homing pro-apoptotic conjugates of the present invention Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule; cytostatic; human. Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide. Score 50; DB 3; Length 13; Pred. No. 3.8; 3; Indels Arap W, Bredesen DE, 3; Mismatches Human breast tumour homing peptide #1. Example 5; Page 89; 176pp; English. AAE06280 standard; peptide; 13 AA. 16-JAN-2001; 2001WO-US001362. Ruoslahti EI, Pasqualini R, 21-JAN-2000; 2000US-00489582 / Match 59.5%; Local Similarity 53.8%; nes 7; Conservative (first entry) 1 CPKVCPRECESNC 13 | : ||| |:| | CGRECPRLCQSSC 13 (BURN-) BURNHAM INST. WPI; 2001-451901/48. WO200153342-A1. Sequence 13 AA; sapiens. 25-SEP-2001 26-JUL-2001 AAE06280; Query Match Homo Matches RESULT 12 **AAE06280** 8888888888888888 8 셤 The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1 (X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from - (L1)C-F1, -(L1)C-P1, -(L2)d-P2, -(L1)C-P1.

(L2)d-P2-(L3)e-P³, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC (L2)d-P2-(L3)e-P³, and L4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, CC c, d, e, and f = are each independently 0 or 1, provided that at least 1, CC d and b is 1. The composition can have cytostatic, antiasthmatic, chrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, chrombosis, or autoimmune diseases. The use of an FC domain (rather than a FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent mucleocides and amino acid sequences used in the composition of the present invention ö Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases. Gaps Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; human. . 0 Score 50; DB 3; Length 13; Pred. No. 3.8; 3; Indels Pasqualini R, Ruoslahti EI; 3; Mismatches Human breast tumour homing peptide #2. Claim 39; Page 557; 608pp; English. AAB21702 standard; peptide; 13 AA. 59.5%; 21-JAN-2000; 2000WO-US001602 99US-00235902 22-MAR-2001 (first entry) Ellerby HM, Bredesen DE, 1 CPKVCPRECESNC 13 | : ||| |:|:| 1 CGRECPRLCQSSC 13 Local Similarity 53.8 tes 7; Conservative (BURN-) BURNHAM INST WPI; 2000-350702/30.

Ellerby HM;

Sequence 13 AA;

Gaps

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Length 13; Indels

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The invention relates to a composition comprising an integrin/adhesion antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are compounds on laminin or saw-scaled viper echistatin and target integrin, selectin or vinculin. Also included are compounds of formula (Ia) and their multimers (X1) a-F¹-(X²) b where; F¹ = Fc domain; X¹ and X² = (I²¹) c-P¹-(I²¹) a-F¹-(I²²) d-P²-(I²¹) e-P²-(I²²) e-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quickly in vivo). The present sequence is an antagonist peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory; immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper; echistratin; integrin; selectin; vinculin; platelet aggregation; angiogenesis; tumour; inflammation; autoimmune disease; rheumatoid arthritis; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition comprising integrin or adhesion antagonistic peptide and vehicle, useful for treating or preventing platelet aggregation, has longer half-life than free peptide.
Score 50; DB 4;
Pred. No. 3.8;
                                                 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrin-antagonist peptide #11.
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                                                                                                                                                                                                                                                                             AAU81104 standard; peptide; 13
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59.5%;
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03-MAY-2000; 2000US-0201394P.
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CGRECPRLCQSSC 13
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                                                   7; Conservative
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  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC
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                                                      Matches
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59.5%; Score 50;

Sequence 13 AA;

Query Match

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The present invention describes a vehicle-peptide molecule (1) or its multimers. (1) can have antininflammatory, antitumour, immunosuppressive, cytostaric, antirhenumatic, antiarchritic, antidiabetic, ophthalmological, antianaemic, anorectic, antininfertility, hemostaric, dermatological, cantianaemic, anorectic, antininfertility, hemostaric, dermatological and neuroprotective activities. (1) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (1) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (1) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, infertility, and neurological degenerative diseases, (1), comporters, infertility, and neurological degenerative diseases, (1), comporters, infertility, and neurological degenerating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating disorders characterised by low megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet tumour which result in thrombocytopaenia, spistemic lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TPO; tumour necrosis factor alpha inhibitor; TPO; tumour nemargonist; IL-1 antagonist; TPO mimetic peptide; EPO mimetic peptide; EPM; VEGF antagonist; TPO mimitic peptide; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antitheumatic; antiarthritic; antidiabetic; ophthalmological; antianemmic; antinflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia;
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
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                         Indels
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M
  Pred. No. 3.8;
                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Integrin binding peptide SEQ ID NO:1071.
                                                                                                                                                                                                                        ABB72956 standard; peptide; 13 AA.
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53.8%;
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                                                                                                             1 CGRECPRICOSSC 13
                      Conservative
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Best Local Similarity
Matches 7; Conserv
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Gaps

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Indels

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fragment where a protein has been inserted into, or replaces a portion of a heavy chain or light chain variable regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ligand binding region (LBR) The present invention describes human mimetibodies, including modified immunoslobulins and cleavage products that can be useful in gene therapy and the generation of transgenic preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is an integrin binding peptide sequence used to make a
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 represent amino acid and nucleic acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to novel mammalian CDR mimetibodies, specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
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                                                                                                                                                                                                           Score 50; DB 5; Length 13; Pred. No. 3.8; 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ73110 standard; peptide; 13 AA.
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                                                                                                                                              Sequence 13 AA;
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59.5%; Score 50; DB 7; Length 13;

mimetibody of the invention

Sequence 13 AA;

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  Pred. No. 3.8;
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Sequence 6738, Ap
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-659-786-2
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US-09-270-767-5784
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US-09-270-767-6105
US-08-37-210A-1
US-09-113-825-1
US-09-113-825-1
US-09-113-825-1
US-08-893-232-1
US-08-893-232-1
US-09-121-457-1
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20000000000000000000000000000000000000	ESULT 1  S-09-139-802-2 Sequence 2, Application US/09139802 Patent No. 6180084 APPLICANT Nosbathi, Erki APPLICANT: Ruoslahti, Erki APPLICANT: Ruoslahti, Erki TITLE OF INVENTION: Molecules That Hor TITLE OF INVENTION: Same TITLE OF INVENTION: Same TITLE OF INVENTION: Same TITLE REFERENCE: P-LJ 3203 CURRENT APPLICATION NUMBER: US/09/139 CURRENT FILING DATE: 1998-08-25 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1996-09-10 SEQ ID NO 2 LENGTH: 13 TYPE: PAT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Peptide	Similarity 53. 7; Conservative CPKVCPRECESNC 1	SULT 2 :-09-659-786-2 Sequence 2, Application US/09659786 Batent No. 6491894 GENERAL INFORMATION: APPLICANT: Ruoslahti, Erkki APPLICANT: Rasqualini, Renata TITLE OF INVENTION: MGR Receptor TITLE OF INVENTION: Molecules Tha TITLE OF INVENTION: Same FILE REFERENCE: P-LJ 3203 CURRENT APPLICATION NUMBER: US/09/CURRENT FILING DATE: 2000-09-11
ব ব ব ব ব ব ব ব ব ব ব ব ব ব ব ব র র র র	SULT 1  -09-139-802-2 Sequence 2, Applicat Patent No. 6180084 APPLICANT: Rucelaht APPLICANT: Rucelaht APPLICANT: Rucelaht APPLICANT: Pasquali TITLE OF INVENTION: TITLE OF INFORMATION: COTHER INFORMATION: OTHER INFORMATION:	-802- atch cal S 1	SULT 2 -09-659-786-2 Sequence 2, Applicat Sequence 2, Applicat Settin No. 6491894 GENERAL INFORMATION: APPLICANT: Rucelah APPLICANT: Pasqual TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: P- CURRENT APPLICATION CURRENT FILING DATE
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RESULT 4
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APPLICANT: Ruoslahti, Erkki
APPLICANT: Raganalini, Renata
APPLICANT: Paganalini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic JOTHER INFORMATION: Peptide US-09-659-786-2
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Pred. No. 0.88;
3; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR PILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Wer. 2.0
SEQ ID NO 2
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08926914
Patent No. 6576239
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                                                                                                                                                                                       ORGANISM: Artificial Sequence
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1 CGRECPRICQSSC 13
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGRECPRICOSSC 13
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-926-914-2
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                                                                                                                                                                      TYPE: PRT
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Sequence 1071, Application US/09428082B
Sequence 1071, Application US/09428082B
Sequence 1071, Application US/09428082B
Seneral INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: CHEETHAM, JANET C.
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
SOFFWARE: PALCALION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-33
SOFFWARE: PALCALION VERSION 3.1
SEQ ID NO 1071
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 4; Length 13;
Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
TYPP: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB Pred. No. 9.7; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-09-428-0828-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 57784, Application US/09270767; Patent No. 6703491
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Patent No. 6639063
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPKVCPRECESNC 13
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-621-976-6330
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Gaps

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Indels

2;

Mismatches

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2;
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                                                  1 CPKVCPRECESNC 13
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86 CQTKCPEKCRNNC 98
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          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                          US-08-537-210A-1
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          Matches
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Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT PALLION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 42488

LENGTH: 118
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; Sequence 105 Application US/08857076C
; Patent No. 6225120
; GENERAL INFORMATION:
    APPLICANT: Ruvkun, Gary
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ruvkun, Garth
; APPLICANT: Paradis, Suzanne
; APPLICANT: Paradis, Suzanne
; APPLICANT: Paradis, Suzanne
; APPLICANT: Paradis, Suzanne
; APPLICANT: Morris, Jason
; APPLICANT: Morris, Jason
; APPLICANT: Morris, Jason
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS; TILE REPERENCE: 00786/351001
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS; TILE REPERENCE: 00786/351001
; CURRENT APPLICATION NUMBER: US/08/857,076C
; UNRENT PILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 383
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Pred. No. 44;
                                                                                                                                                                                           Score 47; DB 4; Length 58;
Pred. No. 8.2;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
; CURRENT FILING DATE: 1999-03-17;
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57784
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Drosophila melanogaster US-09-270-767-42488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.0%;
                                                                                                                                                                                           Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                             1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                    35 CARICPREFEPVC 47
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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US-09-270-767-42488
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DD 66 COTKCPERCENC 13

US-60-577-210a.1

US-60-577-210a.1

US-60-577-210a.1

US-60-577-210a.1

US-60-577-210a.1

SEQUENCE 1. Application US/08537210A

PERMINAL PREMINALY

APPLICANT: POTICH, MAIN

APPLICANT: POTICH

APPLI
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US-008-08-590A-19
US-008-19-590A-19
US-008-08-590A-19
Patent No. 5786158
Patent No. 5786116
Patent No. 5786158
Patent No. 5786116
Patent No. 57861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 1; Length 2471;
Pred. No. 3.1e+02;
1; Mismatches 2; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 31-JAN-1994
CLASSIFICATION NUMBER: 18,872
RECASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
FELEPHONE: (212) 869-8864/9741
TELEPHONE: (212) 730-9090
TELEPHONE: (212) 869-8864/9741
TELEPHONE: (212) 869-106
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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Sequence 16, Application US/08185432

Sequence 16, Application US/08185432

Fatent No. 5750652

GENERAL INFORMATION:

APPLICANT: Busseau, Isabelle

APPLICANT: Busseau, Isabelle

APPLICANT: Wu, Tian

APPLICANT: Matsuno, Kenji

TITLE OF INVENTION: BELTEX PROTEINS, INUCLEIC ACIDS, AND

TITLE OF INVENTION: BELTEX PROTEINS, INCRESC AND COMPOSITIONS

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIR & EDMONDS

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                            TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
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OTHER INFORMATION: Highly conserved ankyrin repeat
OTHER INFORMATION: region of No. 6149902ch
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                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFRARE: FRAESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/537,210
FILLING DATE: 29-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 7326
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.8%;
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Ne COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-113-825-1
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1 Sequence 19, Application US/08532384

1 Patent No. 6083904

2 GENERAL INFORMATION:

1 TITLE OF INVENTION: Therapeutic And Diagnostic Methods

1 TITLE OF INVENTION: Therapeutic Acids

1 TITLE OF INVENTION: Nucleic Acids

1 TITLE OF INVENTION: Nucleic Acids

1 TITLE OF INVENTION: Nucleic Acids

1 TITLE OF INVENTION: Therapeutic Acids

2 TITLE OF INVENTION DATA: Therapeutic Acids

2 TITLE OF INVENTION NUMBER: US/08/532,384

7 TITLING DATE: Therapeutic Acids

2 TITLING DATE: Therapeutic Acids

3 TITLING DATE: Therapeutic Acids

4 TITLING DATE: Therapeutic Acids

3 TITLING DATE: Therapeutic Acids

4 TITLING DATE: Therapeutic Acids

5 TATE: Acids 
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                                                                                                                                       54.8%; Score 46; DB 1; Length 2471; 61.5%; Pred. No. 3.1e+02;
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61.5%; Pred. No. 3.1e+02;
usamatches 2; Indels
                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7326-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISCRATION UNDBER: 18,072
REFRENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEFAM: 212 790-9090
TELEFAM: 212 869864/9741
TELEFA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                1368 CPS--PRDCESGC 1378
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LENGTH: 2471 amino acids
                                                                                                                                                                                                                                                                          1 CPKVCPRECESNC 13
                                                                                                                                                                  Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.5-
8; Conservative
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; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
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STRANDEDNESS: siz
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US-08-532-384-19
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                                                                                                                                          Query Match
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US-08-899-232-1 ; Sequence 1, Application US/08899232 ; Patent No. 6436650 ; GENERAL INFORMATION:

1368 CPS--PRDCESGC 1378

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1;
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Qi, Huilin
TILLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-049, 232
CURRENT APPLICATION NUMBER: US/08/899, 232
CURRENT FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2471
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ALTAVATION:
APPLICANT: ALTAVATION: APPLICANT: Q1, H.
APPLICANT: RIGH, M.
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON FILE REFERENCE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT PILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899,232
EARLIER PILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                    Length 2471;
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Pred. No. 3.18+02;
2; Indels
                                                                                                                                                                                                                                                                                                                  Query Match 54.8%; Score 46; DB 4; Length 247
Best Local Similarity 61.5%; Pred. No. 3.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: November 16, 2004, 14:32:12 Job time : 19.7296 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09121457
Patent No. 6692919
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          1 CPKVCPRECESNC 13
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-121-457-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                     November 16, 2004, 14:30:02 ; Search time 60.8302 Seconds (without alignments) 75.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUDLISHER APPLICATIONS AND THE COMB. DEPT. (1) (2012_6/ptodata/1/pubpaa/US07_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US07_NEW_PUB. DEPT.* (2012_6/ptodata/1/pubpaa/US06_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US07_NEW_PUB. DEPT.* (2012_6/ptodata/1/pubpaa/US07_NEW_PUB. DEPT.* (2012_6/ptodata/1/pubpaa/US08_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US08_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US08_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US08_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US08_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US09_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US09_NEW_PUB..DEPT.* (2012_6/ptodata/1/pubpaa/US09_NEW_PUB..DEPT.* (2012_6/ptodata/1/pubpaa/US108_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US108_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US108_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US108_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US108_PUBCOMB. DEPT.* (2012_6/ptodata/1/pubpaa/US11_NEW_PUB..DEPT.* (2012_6/ptodata/1/pubpaa/US11_NEW_PUB..DEPT.* (2012_6/ptodata/1/pubpaa/US11_NEW_PUB..DEPT.* (2012_6/ptodata/1/pubpaa/US10_PUBCOMB..DEPT.* (2012_6/ptodata/1/pubpaa/US0_NEW_PUB..DEPT.* (2012_6/ptodata/1/pubpaa/U
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1568699 seqs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Applications AA:*
                                                                                                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CPKVCPRECESNC 13
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Maximum DB seq length: 2000000000
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84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                Run on:
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	Description	Sequence 127, App	Sequence 48, Appl	Sequence 325327,	Seguence 48817, A	Sequence 123, App	Sequence 2, Appli	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 1071, Ap	Sequence 1071, Ap	Sequence 1071, Ap	Sequence 1071, Ap
SUMMARIES	QI	US-10-363-204-127	US-10-411-910A-48	US-10-425-115-325327	US-10-282-122A-48817	US-10-363-204-123	US-09-765-086-2	US-09-840-277-32	US-10-264-374-2	US-10-375-992-2	US-10-609-217-1071	US-10-632-388-1071	US-10-651-723-1071	US-10-645-761-1071
	DB	16	17	11	15	16	0	0	14	14	15	15	15	15
	Query Match Length DB	13	844	198	762	6	13	13	13	13	13	13	13	13
م <i>ن</i> و	Match	100.0	63.1	60.7	60.7	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5
	Score	84	53	51	51	20	20	20	20	20	20	20	20	20
	No.	1	7	Э	4	ហ	9	7	ω	σ	10	11	12	13

US-10-411-910A-48
; Sequence 48, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INPORMATION:

Sequence 1071, Ap	Sequence 1071, Ap							2	105	Sequence 105, App	e 10	Sequence 52651, A	Sequence 52367, A				_	Sequence 726, App	•••	•••	_	_				Sequence 43605, A		Sequence 291729,			Sequence 208114,
US-10-666-696-1071	US-10-653-048-1071	US-10-264-374-2	US-10	US-10	US-10-425-	US-09	US-10-264-237-2213		US-09-205-658-105	₽		US-10-282-122A-5		US-09-950-933A-52	Þ			US-10	US-10	US-10	US-10-720-	US-1	US-1		US-1	US-1	US-10	US-10-425	US-10-425	US-10-739-930-	US-10-425-115-208114
	15	15	16	16	17	10					Н	15	Н	<u>م</u>				16												-	11
H	13	H	H	1594	7	12]	13	Ę,	38	383	38	46	470	10	236	237	1015	2203	2469	2469	2471	8	119	145	145	152	235	245	9		349
59.5	59.5	59.5	59.5	59.5	57.1	57.1	57.1	56.0	56.0	56.0	56.0	56.0	56.0	54.8	54.8	54.8	54.8	54.8				53.6							53.6		53.6
20	20	20	20	20	48	48	48	47	47	47	47	47	47	46	46	46	46	46	46	46	46	45	45	45	45	45	45	45	45	45	45
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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RESULT 1

US-10-363-204-127

US-10-363-204-127

Sequence 127, Application US/10363204

Publication No. US20040170955A1

Sequence 127, Application Wo. US20040170955A1

SEQUENCE INVENTION:

APPLICANT: Board of Regents, The University of Texas System;

TITLE OF INVENTION:

APPLICANT: Board of Regents, The University of Texas System;

TITLE OF INVENTION:

TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display of Texas Statements of System;

CURRENT FILING DATE: 2003-03-07

CURRENT FILING DATE: 2003-03-07

SOFTWARE: PATOME: Patentin version 3.1

SEQ ID NO 127

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

PATOME: NAME/KEY: Peptide

OCATION: (1)...(13)

CONTER INFORMATION: synthetic construct

QUESTION: (1)...(13)

MANGE/KEY: Peptide

OUGSTION: (1)...(13)

MATCHES 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE ICPKVCPRECESNC 13

ON ICPKVCPRECESNC 13
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LOCATION: (1)..(9)
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bacteroides fragilis
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 CGRVCPQEKQCESKC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPKVCPRE--CESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.9
Matches 8; Conservative
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    Forsyth, R.
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NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-282-122A-48817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-363-204-123
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; Publication No. US20040214272A1
; Publication No. US20040214272A1
; Fublication No. US20040214272A1
; GAPPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
; APPLICANT: Cano, Yongwei
; APPLICANT: APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325327
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APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
FILE REFERENCE: H2041203-P
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52;
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Pred. No. 29;
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                                                                                                                                                                                                                                                                                                   4; Indels
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US-10-425-115-325327
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                       CURRENT APPLICATION NUMBER: US/10/411,910A
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                              Score 53;
Pred. No.
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                                                                                                                                                                              TYPE: PRT ORGANISM: Desulfitobacterium hafniense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
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53.8%;
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177 CGRVCPHSCEAQC 189
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Best Local Similarity 53.5-
Transport Conservative
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Best Local Similarity 53.8°
Matches 7; Conservative
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ORGANISM: Zea mays
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                                                                                                                                         SEQ ID NO 48
LENGTH: 844
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Sequence 123, Application US/10363204
Sequence 123, Application US/10363204
Publication No. US20040170955A1
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT
CURRENT PILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 123
LENGTH: 9
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APPLICAT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITAA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 06/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/203,23

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-
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Sequence 2, Application US/10264374;
Sequence 2, Application US/10264374;
Publication No. US20030113320A1
GENERAL INFORMATION:
APPLICANT: RUOSIANLI, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/10/264,374
CURRENT FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1996-09-10
PRIOR FILING DATE: 1996-09-10
PRIOR FILING DATE: 1996-09-10
SEQ ID NO 2
LENGTH: 13
TURNEL PATENTIN VET. 2.0
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
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Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
Derived Therefrom, and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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Pred. No. 4.1;
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ADDRESSE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
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REPLICATION NUMBER: US/10/375,992
FILING DATE: 27.Feb-2003
CLASSIFICATION: 435
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Publication No. US20030152578A1
GENERAL INFORMATION:
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Best Local Similarity 53.0-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-264-374-2
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                                                                                                                                        APPLICANT: Pasqualli, Renata
APPLICANT: Wadih, Arap
APPLICANT: Wadih, Arap
APPLICANT: Bredesen, Dale E.
APPLICANT: Bredesen, Dale E.
APPLICANT: Bredesen, Dale E.
APPLICANT: Bredesen, Dale E.
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apoptotic Activity
FILE REFERENCE: P-Li 3844
CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 235
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FEIGE, ULRICH
APPLICANT: FEIGE, ULRICH
APPLICANT: LACEY, DAVID LEB
APPLICANT: LACEY, DAVID LEB
APPLICANT: LACEY, DAVID LEB
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
FILE REFERENCE: A-688A
CURRENT APPLICATION NUMBER: 00/198,919
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR APPLICATION NUMBER: 60/201,394
PRIOR FILING DATE: 2000-04-21
PRIOR PILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 135
SOFTHARR: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-32
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; OTHER INFORMATION: synthetic peptide
US-09-765-086-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32, Application US/09840277
Patent No. US20020168363A1
                                             Sequence 2, Application US/09765086; Patent No. US20010046498A1
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 53.8%;
Matches 7; Conservative
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1 CGRECPRLCOSSC 13
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1 CGRECPRLCQSSC 13
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Best Local Similarity 53.8
Matches 7; Conservative
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US-09-840-277-32
RESULT 6
US-09-765-086-2
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LENGTH: 13
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3; Mismatches
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CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR PLING DATE: 1999-10-22
                                                                                                                                                                                                                                  Score 50;
Pred. No. 4
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Publication No. US20040057953A1
GENERAL INFORMATION:
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1071
LENGTH: 13
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative 3
                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 53.6-
Best Local 7; Conservative
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US-10-645-761-1071
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APPLICANT: FIGURA.PA
APPLICANT: LIU, CHUAN-PA
APPLICANT: LIU, CHUAN-PA
APPLICANT: HOWERTHM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT PELING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR PILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE PELING DATE: 1991-10-23
NUMBER OF SEQ ID NOS: 1133
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Publication No. US20040053845A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: CHECTHAM, JANET C.
APPLICANT: BOOME, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                        Score 50, DB 14; Length 13;
Pred. No. 4.1;
3; Mismatches 3; Indels
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CURRENT APPLICATION NUMBER: US/10/632,388
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/9/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
                                                                                                              TYPE: amino acid

TYPE: amino acid

TOPOLOGY: both

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-375-992-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1071, Application US/10609217
Publication No. US20040044188A1
GENERAL INFORMATION:
                          E: (619) 535-9001
(619) 535-8949
      TELECOMMUNICATION INFORMATION
                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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1 CGRECPRLCQSSC 13
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US-10-632-388-1071
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LENGTH: 13
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APPLICANT: LIU, CHUAN-RA
APPLICANT: LIU, CHUAN-RA
APPLICANT: LIU, CHUAN-RA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
CURRENT FILING DATE: 2003-08-29
CURRENT FILING DATE: 2003-08-29
PRIOR PELLING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
SECOND NOS: 1133
SOFTWARE: PATENTING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PATENTING VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1071, Application US/10645761
Publication No. US20040071712A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: CHEFTHAM, JANET C.
APPLICANT: GREFTHAM, JANET C.
APPLICANT: GRONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.5%; Score 50; DB 15; Length 13; 53.8%; Pred. No. 4.1;
DB 15; Length 13;
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Publication No. US20040077022A1

GENERAL INFORMATION:
APPLICANT: FEIGE, UIRICH
APPLICANT: CHEETHAM, JANET C.
APPLICANT: CHEETHAM, JANET C.
APPLICANT: GUDAS, THOMAS CHARLES
APPLICANT: GUDAS, THOMAS CHARLES
APPLICANT: GUDAS, JANEM ASIE
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REPERBRUES: A-527A
CURRENT APPLICATION WUMBER: US/10/666,696
CURRENT APPLICATION NUMBER: US/09/563,286C
PRIOR FILING DATE: 2003-09-19
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1157
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1071
LENGTH: 13
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Sequence 1071, Application US/10653048

Publication No. US20040087778A1

GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH

APPLICANT: LIU, CHUAN-FE

APPLICANT: LIU, CHUAN-FE

APPLICANT: BOONE, THOMAS CHARLES

TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-S7;

CURRENT APPLICATION NUMBER: US/10/653,048

CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US/09/428,082B

PRIOR FILING DATE: 1999-10-22
                                                                                                                                                                                                                         Score 50; DB 15; Length 13; Pred. No. 4.1; 3; Indels 3; Indels
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Pred. No. 4.1;
3; Mismatches
                                                                                          ; TYPE: PRT; ORGANISM: Artificial Sequence; PEATURE: ; PEATURE; US-10-645-761-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-10-666-696-1071
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 1071
LENGTH: 13
                                                                                                                                                                                                                         Query Match 59.5%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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CGRECPRICOSSC 13
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prior Application Number: 60/105,371

prior Filing Date: 1998-10-23

number of SEQ ID NOS: 1133

software: Patentin version 3.1

software: Patentin version 3.1

software: Patentin version 3.1

trips: PRT

profile: PRT

profile
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Title:

Run

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November 16, 2004, 14:19:17; Search time 212.17 Seconds (without alignments) 67.889 Million cell updates/sec
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2: /cgn2 6/ptodata/1/paa/USO6_COMB.pep:*
4: /cgn2 6/ptodata/1/paa/USO6_COMB.pep:*
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28: /cgn2 6/ptodata/1/paa/USO99A_COMB.pep:*
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/ Cgn2 = 6/ptodata/1/paa/US102 = COMB.pep:

/ Cgn2 = 6/ptodata/1/paa/US103 = COMB.pep:

/ Cgn2 = 6/ptodata/1/paa/US104 = COMB.pep:

/ Cgn2 = 6/ptodata/1/paa/US105 = COMB.pep:

/ Cgn2 = 6/ptodata/1/paa/US105 = COMB.pep:

/ Cgn2 = 6/ptodata/1/paa/US108 = COMB.pep:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6730630 seqs, 1107998698 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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84
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 3, Appli Sequence 8, Appli Sequence 5704, Ap Sequence 5582, Ap Sequence 5583, Ap Sequence 5898, Ap Sequence 5573, Apply Sequence 325327, Apply Sequence 5784, Apply Sequence 6897, Apply Sequence 6, Apply Sequence 123, Apply Sequence 123, Apply Sequence 123, Apply Sequence 123, Apply Sequence 56, Apply Sequence 26, Apply Sequence 27, Appli 1071, Ap 1071, Ap 2, Appli Sequence 127, App Sequence 48, Appl Sequence 48, Appl Sequence 92086, A Appli Appli , Appl Sequence 5, Appli Sequence 2, Appli Sequence 1027, Ap Sequence 1071, Ap 1071, Sequence 2, Sequence 32, Sequence 32, Description Sequence Sequence 2 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence В Query Match Length 63.1 63.1 Score Result No. 

#### ALIGNMENTS

PCT-US01-27692A-127

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Sequence 127, Application PC/TUS0127692A
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774-P003PCT
CURRENT APPLICATION NUMBER: PCT/US01/27692A
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 251
SEQ TWARE: Patentin version 3.1
SEQ ID NO 127
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Peptide
J. CCATION: (1)...(13)
COTHEN INFORMATION: synthetic construct
PCT-US01-27692A-127
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Gaps
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                                                                                                                                                                                                                          Sequence 3, Application US/10784537

Sequence 3, Application US/10784537

GENERAL INFORMATION:
APPLICANT: PARCHIO.
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: MACHIO, SERENA
APPLICANT: MACHIO, SERENA
TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: POR THE TREATMENT OF CANCER
FILE REFERENCE: UTSC:872US
CURRENT APPLICATION NUMBER: US/10/784.537
CURRENT FILING DATE: 2004-02-23
FRIOR PILING DATE: 2001-09-07
FRIOR FILING DATE: 2001-09-07
FRIOR FILING DATE: 2001-09-08
FRIOR PILING DATE: 2001-09-08
FRIOR FILING DATE: 2001-09-08
FRIOR FILING DATE: 2000-09-08
FRIOR FILING
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APPLICANT: PASGUALINI
APPLICANT: MARCHIO, SERENA
APPLICANT: LAHDENRANTA, JOHANNA
APPLICANT: LAHDENRANTA, JOHANNA
TITLE OF INVENTION: AMINOPEPITIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
FILE REFERENCE: UTSC:872US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 84; DB 33; Length 13; 100.0%; Pred. No. 0.00018; tive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/784,537

CURRENT FILING DATE: 2004-02-23

PRIOR APPLICATION NUMBER: PCT/US02/27836

PRIOR PLING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: PCT/US01/27692

PRIOR PLING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: 60/231,266

PRIOR FILING DATE: 2000-09-08

PRIOR PLING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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Matches 13; Conservative
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US-10-784-537-3
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APPLICANT: only)
APPLICANT: wolvi)
APPLICANT: America only)
APPLICANT: America only)
TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
TITLE OF INVENTION: and Adipose Tissues
FILE REFERENCE: 5774.P009PCT
CURRENT APPLICATION NUMBER: PCT/US02/27836
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 2001-09-07
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APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REPERBNCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 127
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60, Application PC/TUS0227836
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: purposes of all designated states except US)
APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
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100.0%; Score 84; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels
                              100.0%; Score 84; DB 1; Length 13; 100.0%; Pred. No. 0.00018; Live 0; Mismatches 0; Indels
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COATION: (1)..(13)

OTHER INFORMATION: synthetic construct

US-10-363-204-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Peptide PCT-US02-27836-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-10-333-204-127
Sequence 127, Application US/10363204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 13
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FEATURE:
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                      1 CPKVCPRECESNC 13
                                                                                                                                                                                    1 CPKVCPRECESNC 13
                                      Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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PCT-US02-27836-60
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JS-60-581-351-5583
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US-60-581-351-5898
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US-60-581-351-5704
US-60-581-351-5704
S. Sequence 5704, Application US/60581351
S. Sequence 5704, Application US/60581351
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
TITLE OF INVENTION NUMBER: US/60/581,351
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-60-581-351-5582

Sequence 5582, Application US/60581351

GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
TITLE OF INVENTION NUMBER: US/60/581,351

CURRENT APPLICATION NUMBER: US 60/479,962

PRIOR PRILING DATE: 2003-06-19

NUMBER OF SEQ ID NOS: 13980

SOFTWARE: Patentin version 3.2

LENGTH: 464
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                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-784-537-8
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Pred. No. 0.024;
0; Mismatches 0; Indels
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Pred. No. 50;
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US-60-581-351-5704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Thermoanaerobacter tengcongensis
US-60-581-351-5582
                                  TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                   Query Match 81.5%;
Best Local Similarity 92.3%;
Matches 12; Conservative
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159 CGRVCPHTCESQC 171
                                                                                                                                                                                                                                              1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                    1 CPKVCPREC-SNC 12
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 500
SEQ ID NO 8
LENGTH: 12
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)B
FILE REFERENCE: 38-21(53372)B
CURRENT PAPLICATION WUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION WUMBER: US 60/479,962
NUMBER OF SEQ ID NOS: 13980
SOFWARE: Patentin Version 3.2
SEQ ID NOS: 13980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REPERENCE: 38-21(53372)
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR PELING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 649
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Sequence 5795, Application US/60581351
GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REPERENCE: 38-21 (53372)B
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT PAPLICATION NUMBER: US 60/479,962
PRIOR APPLICATION NUMBER: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SEQ ID NO 5795
LENGTH: 672
TYPE: PRI
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Pred. No. 1.2e+02;
1; Mismatches 4; Indels
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; ORGANISM: Thermoanaerobacter tengcongensis
US-60-581-351-5583
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GENERAL INFORMATION:
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; ORGANISM: Wolinella succinogenes
US-60-581-351-5898
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Matches 9; Conservative
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US-10-425-115-325327
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GENERAL INFORMATION:
APPLICANT: Solazyme, Inc.
TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
TITLE OF INVENTION: Production
TITLE OF INVENTION: Production
FILE REFERENCE: H204101-CTP
CURRENT APPLICATION NUMBER: US/10/763,712A
CURRENT FILING DATE: 2004-01-21
PRIOR PILING DATE: 2002-11-04
PRIOR PILING DATE: 2003-04-12
PRIOR PILING DATE: 2003-04-12
PRIOR PILING DATE: 2003-04-12
PRIOR PILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PetentIn version 3.2
SEQ ID NO 4.2
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Sequence 48, Application US/10411910A
GENERAL INFORMATION:
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
FILE REFERENCE: H2041203-P
CURRENT APPLICATION NUMBER: US/10/411,910A
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
LENGTH: 844
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Pred. No. 1.5e+02;
2; Mismatches 4; Indels
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Pred. No. 1.5e+02;
2; Mismatches 4; Indels
                                                        Score 53; DB 36; Length 672;
Pred. No. 1.2e+02;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Desulfitobacterium hafniense US-10-411-910A-48
; ORGANISM: Geobacter metallireducens
US-60-581-351-5795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.1%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                          63.1%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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177 CGRVCPHSCEAQC 189
                                                                                                                                                                203 CGRVCPHPCETHC 215
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US-10-763-712A-48
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US-10-411-910A-48
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ORGANISM:
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RESULT 13

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Sequence 92086, Application US/09791537

Sequence 92086, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
SOFTWARE: Patentin version 3.0
SEQ ID NO 92086
LENGTH: 413
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Sequence 325327, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFRENCE: 38-21 (53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369327
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GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: UNcleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)8
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: PatentIN version 3.2
SEQ ID NO 5573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.9%; Score 52; DB 22; Length 413; Best Local Similarity 53.3%; Pred. No. 1.1e+02; Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.9%; Score 52; DB 36; Length 413; 53.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Rhodobacter sphaeroides US-60-581-351-5573
                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Rhodobacter sphaeroides US-09-791-537-92086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CPKVCP--RECESNC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CPKVCP--RECESNC 13
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Best Local Similarity 53.3%
Best Local Similarity 53.3%
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o;
                                                                                                                                                                                                   Query Match 60.7%; Score 51; DB 30; Length 198;
Best Local Similarity 53.8%; Pred. No. 79;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps
) ORGANISM: Zea mays
; FRATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FRATURE:
; OTHER INFORMATION: Clone ID: MRT4577_5976C.1.pep
US-10-425-115-325327
                                                                                                                                                                                                                                                                                           1 CPKVCPRECESNC 13
||| || :| :|
76 CPKTCPNKCLAFC 88
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Search completed: November 16, 2004, 14:46:43 Job time : 213.17 secs

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Sequence 14, Appl Sequence 1617, Appl Sequence 1617, Appl Sequence 4, Appli Sequence 6, Appli Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 161, Ap Sequence 161, Ap Sequence 1594, A Sequence 1594, A Sequence 1594, A Sequence 1594, A

Sequence 15951, A Sequence 27094, A Sequence 14192, A Sequence 119, App

US-10-220-366A-15700

ALIGNMENTS

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APPLICANT: PASODALINE ET AL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
TITLE OF INVENTION: DATACENTA AND ADIPOSE TISSUES
FILE REPERENCE: UTSC: 855GUS
CURRENT PAPLICATION NUMBER: US/10/489,071
CURRENT FILING DATE: 2004-03-08
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PATENTI VERSION 3.1
SEQ ID NO SB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-363-374-14

US-10-220-366A-16237

US-10-965-357-4

US-10-965-357-4

US-10-965-357-6

US-10-967-851-4

US-10-967-851-4

US-10-967-851-6

US-10-967-851-6

US-10-967-851-6

US-10-967-851-8

US-10-20-366A-15949

US-10-20-366A-15949

US-10-20-366A-15949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 198; DB 6; Best Local Similarity 100.0%; Pred. No. 7.4e-15; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                            US-10-220-366A-15951
US-10-220-366A-27094
US-10-732-923-14192
                                                                                                                                                                                                                                US-10-967-702-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Oryza sativa (indica cultivar-group)
US-10-732-923-15015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic Peptide US-10-489-071-58
                                                                                                                                                                                                                                                                                                        RESULT 1

US-10-489-071-58

; Sequence 58, Application US/10489071

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
RESULT 2
US-10-732-923-15015
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Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 15841, A
Sequence 146, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14191, A
14210, A
20601, A
14190, A
8, Appl
4, Appli
13624, A
29, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, App)
Sequence 15015, 1
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                                                                                  November 16, 2004, 14:24:42; Search time 14.0377 Seconds (without alignments) 40.083 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2 6/ptodata/1/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/1/paa/US06 NEW COMB.pep:*

3: /cgn2 6/ptodata/1/paa/US07 NEW COMB.pep:*

4: /cgn2 6/ptodata/1/paa/US08 NEW COMB.pep:*

5: /cgn2 6/ptodata/1/paa/US08 NEW COMB.pep:*

6: /cgn2 6/ptodata/1/paa/US10 NEW COMB.pep:*

7: /cgn2 6/ptodata/1/paa/US11 NEW COMB.pep:*

8: /cgn2 6/ptodata/1/paa/US11 NEW COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-489-071-58

US-10-732-923-15015

US-10-874-049-1

US-10-874-049-1

US-10-820-366A-18045

PCT-US04-33017-4

US-10-95-128-4

US-10-95-952-146

US-10-955-952-146

US-10-955-952-146

US-10-955-952-146

US-10-955-952-14191

US-10-772-923-14191

US-10-732-923-14190

US-10-732-923-14190

US-10-732-923-14190

US-10-732-923-14190

US-10-732-923-14190

US-10-153-604B-89

US-10-153-604B-89

US-10-153-604B-89

US-10-153-604B-89
                                                                                                                                 US-10-784-537-1
198
1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
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US-10-966-673-75
US-10-399-103A-851
US-10-874-049-3
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      80665 seqs, 18150633 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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99445
99445
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133
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Perfect score:
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56.5
56.5
56.5
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Maximum DB
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                                                                                     Run on:
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No.
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Gaps

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Length 31; Indels

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US-10-220-366A-18045
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APPLICANT: Shen, Annie
APPLICANT: Shen, Annie
APPLICANT: Seri, Annie
APPLICANT: Sevilla, Blizabeth
APPLICANT: Sevilla, Blizabeth
APPLICANT: Aspelund, Amy
TITLE OF INVENTION SUBJECTOR B Adenovirus Vectors for Treating Disease
FILE REPERENCE: ONYX 1053-ORD
CURRENT APPLICATION NUMBER: US/10/874,049
CURRENT FILING DATE: 2004-06-22
PRIOR PLING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                            APPLICANT: Shen, Jerry Yuqiao
APPLICANT: Shen, Jerry Yuqiao
APPLICANT: Shen, Jerry Yuqiao
APPLICANT: Sevilla, Annie
APPLICANT: Sevilla, Elizabeth
APPLICANT: Sevilla, Elizabeth
APPLICANT: Sepillad, Any
TITLE OF INVENTION: Subgroup B Adenovirus Vectors for Treating Disease
FILE REFERENCE: ONYX 1053-ORD
CURRENT APPLICATION NUMBER: US/10/874,049
CURRENT FILING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: US 60/488678
PRIOR FILING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.3
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                                                     Gaps
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     DB 6; Length 895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.3%; Score 66; DB 6; Length 35823; Best Local Similarity 44.4%; Pred. No. 1.1e+02; Matches 12; Conservative 2; Mismatches 13; Indels
                                                  Indels
                                                                                                                              647 YNPC--GCQQMCGKDCACVENGTCCEKYCGCSKSC 679
                                                                                               2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC 31
     Score 67.5; DB
Pred. No. 3.1;
3; Mismatches
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                                                                                                                                                                                                                                                                      Sequence 1, Application US/10874049 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/10874049; GENERAL INFORMATION:
Query Match
Best Local Similarity 45.7%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 39.34
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-874-049-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 35346
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LENGTH: 35823
                                                                                                                                                                                                                                               US-10-874-049-1
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Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Massachusetts
APPLICANT: CZECH, Michael P.
APPLICANT: CZECH, Michael P.
APPLICANT: CRONIN, Thomas
TITLE OF INVENTION: PLEKSTRIN HOMOLOGY DOMAINS AND USES THEREFOR
TITLE OF INVENTION: VMNBER: PCT/US04/33017
CURRENT APPLICATION NUMBER: PCT/US04/33017
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-07
FRIOR FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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Pred. No. 70;
2; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.5%; Score 58.5; DB 6; Length 143; Best Local Similarity 35.5%; Pred. No. 5.2; Matches 11; Conservative 3; Mismatches 14; Indels
Sequence 18045, Application US/10220366A

Sequence 18045, Application US/10220366A

GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042

CURRENT APPLICATION NUMBER: US/10/220,366A

CURRENT FILING DATE: 2002-08-28

PRIOR APPLICATION NUMBER: 09/577,409

PRIOR PILING DATE: 2000-05-18

PRIOR PLING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 27802

SOFTWARE: Custom

SEQ ID NO 18045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i LOCATION: (1)...(143)
i OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-18045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
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; Sequence 4, Application US/10962128
; GENERAL INFORMATION:
APPLICANT: LAMBRIGHT, David G.
; APPLICANT: CZECH, Michael P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.5%;
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Best Local Similarity 45.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Gaps

7

Indels

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APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TILLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330RALI2

CURRENT PELING DATE: 2030-40-29

PRIOR PILING DATE: 1997-60-12

PRIOR PELING DATE: 1997-60-18

PRIOR PILING DATE: 1997-60-18

PRIOR PILING DATE: 1997-60-18

PRIOR PILING DATE: 1997-60-17

PRIOR PILING DATE: 1997-60-17

PRIOR PLILING DATE: 1997-60-17

PRIOR PLILING DATE: 1997-60-17

PRIOR PLILING DATE: 1997-60-17

PRIOR PLILING DATE: 1997-00-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR PLILING DATE: 1997-00-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR PLILING DATE: 1997-00-17

PRIOR PLING DATE: 1997-00-17

PRIOR PLILING DATE: 1997-00-19

PRIOR PLILING DATE: 1997-00-19

PRIOR PLILING DATE: 1997-00-19

PRIOR PLILING DATE: 1997-00-19

PRIOR PLILING DATE: 1997-00-19
                                                                                                                                                                                                                                                                                                               27.8%; Score 55; DB 6; Length 119; 37.0%; Pred. No. 10;
                                                                                                                                         FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(119)

OTHER INFORMATION: Kaa = any amino acid or nothing
US-10-220-366A-14903
                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 cvrvcacvc--scacgcrcvtxmslac 118
                                                                                                                                                                                                                                                                                                                                                                                                                                    5 CIRECESICGADGACWTWCADGCSRSC 31
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Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart, Timothy A. Tumas, Daniel
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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                       SEQ ID NO 14903
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapien
US-10-955-952-146
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 10; Conserva
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-955-952-146
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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                    TITLE OF INVENTION: VARIANT POLYPEPTIDES CONTAINING
TITLE OF INVENTION: PLEKSTRIN HOMOLOGY DOMAINS AND USES THEREFOR
FILE REPERENCE: UMY-086
CURRENT APPLICATION NUMBER: US/10/962,128
CURRENT FILING DATE: 2004-10-07
PRIOR PILLING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILLE REPERENCE: 2127-2-042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
PRIOR PLICATION NUMBER: 09/577,409
PRIOR PLILING DATE: 2000-05-18
PRIOR PLILING DATE: 2000-05-18
PRIOR PLILING DATE: 2001-02-3
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: Custom
SEQ ID NO 15841
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.3%; Score 56; DB 6; Length 123; 29.0%; Pred. No. 8.2;
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NAME/KEY: misc feature
LOCATION: (1)...(123)
OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-15841
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.5%; Score 56.5; Di
45.8%; Pred. No. 70;
tive 2; Mismatches
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; Sequence 15841, Application US/10220366A
; GENERAL INFORMATION:
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Best Local Similarity 29.03
Matches 9; Conservative
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Best Local Similarity 45.8
Matches 11; Conservative
CRONIN, Thomas
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 1602
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APPLICANT:
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Query Match 27.5
Best Local Similarity 40.6
Matches 13; Conservative
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ORGANISM: Homo Sapien
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CURRENT PILING DATE: 1907-06-18

PRIOR FILING DATE: 1997-06-18

PRIOR PLICATION NUMBER: 60/05974

PRIOR PLICATION NUMBER: 60/059113

PRIOR PLICATION NUMBER: 60/059115

PRIOR PLILING DATE: 1997-09-17

PRIOR PLILING DATE: 1997-09-18

PRIOR PLILING DATE: 1997-09-19

PRIOR PLILING DATE: 1997-09-19

PRIOR PLILING DATE: 1997-09-19
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                                                     Gaps
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NUMBER OF SEQ ID NOS: 550
                                                     6
     DB 6; Length 945;
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                                                     Indels
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  Score 54.5; DI
Pred. No. 70;
1; Mismatches
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40.6%; Pred. No. 70;
cive 1; Mismatches
                                                                                                                                                                                                                                                                           Sequence 146, Application US/10157779 GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-09-19
     27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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DeForge,Laura
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Gurney, Austin L.
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Best Local Similarity 40.6
Matches 13; Conservative
Query Match
Best Local Similarity 40.6
Matches 13; Conservative
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; ORGANISM: Homo Sapien
US-10-157-779-146
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APPLICANT: Wacad, William
APPLICANT: Wacad, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3330R1C33
CURRENT APPLICATION NUMBER: US/10/964,241
CURRENT FILING DATE: 2004-10-12
PRIOR PLICATION NUMBER: E0/049911
PRIOR PLILING DATE: 1997-06-18
PRIOR PLILING DATE: 1997-06-18
PRIOR PLILING DATE: 1997-06-18
PRIOR PLILING DATE: 1997-06-18
PRIOR PLILING DATE: 1997-08-26
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-19
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Pred. No. 70;
1; Mismatches 9; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 791CIP4
CURRENT PAPLICATION NUMBER: US/10/972,024
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: PCT/US01/08655
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Sequence 146, Application US/10964241 GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
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; Sequence 14191, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: EGGETCON. Michael D
; TITLE OF INVERTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; RIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; ENGRH: 994
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796) C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 14210
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 945;
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PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-09-22
PRIOR PELING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-24
PRIOR FILING DATE: 2000-10-34
PRIOR PILING DATE: 2000-10-34
PRIOR PILING DATE: 2001-02-1
PRIOR PILING DATE: 2001-02-1
PRIOR PILING DATE: 2001-02-1
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-03-22
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US-10-732-923-14210
; Sequence 14210, Application US/10732923
; GENERAL INFORMATION:
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; ORGANISM: Rattus norvegicus
US-10-732-923-14191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 945
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-972-024-292
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; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-732-923-14210
US-10-732-923-14210

Query Match
Best Local Similarity 30.6%; Pred. No. 79;
Matches 11; Conservative 3; Mismatches 15; Indels 7; Gaps

Qy | CYMIC-----IRECESICGADGACWTWCADGCSR 29
| CYMIC------IRECESICGADGACWTWCADGCSR 29
| Db | 698 CGELCNKLLSCKTHFCEKLCHPDGBCESSCKKECGK 733

Search Completed: November 16, 2004, 14:47:12
Job time: 15.0377 secs
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OM protein - protein search, using sw model

November 16, 2004, 14:15:03; Search time 35.0943 Seconds (without alignments) 84.991 Million cell updates/sec Run on:

US-10-784-537-1 198 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB & Maximum DB & Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	hypothetical prote	nsect		depressant insect	-				hypothetical prote	ë	hypothetical prote	hypothetical prote		polycomb protein E	hypothetical prote		depressant insect	hypothetical prote	protein C24B5.5 [i	ultra-high-sulfur	ultra-high-sulfur	lectin-B - Virgini	probable proteinas	chorion protein -	CT105 hypothetical	hypothetical prote	cal.	epidermal growth f
	36	• E	93	91	31	32	66	00	2	11	51	000	96	- 12	33	7.	2	33	22	9.	9	69	53	1,	디	22	6.0	
· A	00	B34123	\$5209	A61616	T23681	T23682	T22099	T22100	T22102	A21761	T20561	T23680	T27686	T52415	T01503	T32497	A40472	T20283	G89152	B38346	A38346	JC5559	S61553	\$23061	C8654	D72082	T25169	EGRT
08	90	1 (1	7	~	~	~	~	~	~	~	N	~	~	~	~	~	7	7	~	~	~	~	~	~	N	~	7	н
% Query Match Length	654	61	3133	82	1513	294	163	163	164	124	728	372	314	856	868	2150	82	103	328	223	230	295	74	105	258	258	330	1133
% Query Match		33.8	33.1	32.3	32.3	32.1	31.6	31.6	⊣	31.1	30.6	30.3	30.1	30.1	30.1	30.1	29.8	29.8	29.8	29.5	29.5	29.5	29.0	29.0	28.8	28.8	28.8	28.8
Score	ı σ	. 9	65.5	64	64	63.5	62.5	2	N	~	60.5	9	59.5	O	σ	59.5	59	59	59	58.5	58.5	58.5	57.5	57.5	57	57	57	57
Result No.	i	1 M	4	Ŋ	9	7	80	6	10	11	12	13	14		16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical protein K03D10.1 - Caenorhabditis elegans
hypothetical protein K03D10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T23271
R;White, S.
A;Reference number: Z19719
A;Reference number: Z19719
A;Reference number: Z19719
A;Recession: T23271
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recession: T23271
A;Residues: DNA
A;Residues: 1-662 <WIL>
A;Cross-references: UNIPROT:062299; EMBL:Z81561; FIDN:CAB04551.1; GSPDB:GN00019; CESP:K0?
C;Genetics: Looked Company Co

CVQACQPQCQQTCGSNVQCVSACQNSCQQSC 564

534

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35.1%; Score 69.5; DB 2; Length 662; 44.4%; Pred. No. 2;

Query Match Best Local Similarity

A;Gene: CESP:K03D10.1 A;Map position: 1 A;Introns: 23/3; 78/3; 264/3; 597/3

alpha tectorin - c denressant insect-	depressant insect-	regulator protein	Balbiani ring 3 pr	zonadhesin - pig	von Willebrand fac	depressant insect-	hypothetical prote	hypothetical prote	excitatory insect	neurotoxin I' prec	probable expressio	protein R09B5.5 (i	. hypothetical prote	insulin receptor -
T30243	B59352	JE0394	S08167	T34022	VWHU	C59352	T35190	T23802	A59006	NTSR12	T36770	A88949	T29880	T30346
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2120	61	310	1700	2476	2813	61	534	358	19	83	272	388	572	1390
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28.8	8 8	28	28	28	28	28	28	28	27	27	27	27	27	27
57	56.5	56.5	56.5	56.5	56.5	56	26	55.5	22	22	22	22	22	22
30	35	33	34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1
	hypothetical protein C14C11.8 - Caenorhabditis elegans
	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
	C;Accession: T30136 R:Du. Z.: Cattung. S.
	submitted to the EMBL Data Library, March 1996
	A; Description: The sequence of C. elegans cosmid C14C11.
_	A; Reference number: 220742
	A; Accession: T30136
	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A; Molecule type: DNA
	A;Residues: 1-654 <duz></duz>
	A; Cross-references: UNIPROT: Q17982; EMBL: U53141; PIDN: AAA96110.1; GSPDB: GN00023; CESP: C14
	A; Experimental source: strain Bristol N2; clone C14C11
	C;Genetics:
_	A;Gene: CESP:C14C11.8
	A; Map position: 5
-	A;Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3
	Query Match 36.4%; Score 72; DB 2; Length 654;
	b; Pred. No. 1.1;
	Matches 10; Conservative 7; Mismatches 14; indels 0; Caps 0;
	OV 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
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33.1%; Score 65.5; I
46.7%; Pred. No. 16;
iive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CIRECESICGADGACWTW 22
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                          Local Similarity 46.7
tes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
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A;Accession: T23681
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A61616
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Best Local Similarity
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A;Gene: CESP:M02G9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A61616
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  Query Match
Best Local Si
Matches 14;
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C;Species: Bombyx mori (silkworm)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 12-Jul-2004
C;Accession: 552093; 570920
R;Kotani, B; Yamakawa, M.; Iwamoto, S.; Tashiro, M.; Mori, H.; Sumida, M.; Matsubara, F
Biochim. Biophys. Acta 1260, 245-258, 1995
A;Title: Cloining and expression of the gene of hemocytin, an insect humoral lectin which
A;Reference number: S52093; MUID:95178544; PMID:7873598
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-61 <ZLO1>
A;Cross-references: UNIPROT:P19855
R;Kopeyan, C.; Mansuelle, P.; Sampieri, F.; Brando, T.; Bahraoui, E.M.; Rochat, H.; Gran
FEBS Lett. 261, 423-426, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Molecule type: protein
, Residues: 1-61 < KOP>
; Zlotkin, E.; Eitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhart, W.; Fowler,
iochemistry 30, 4814-4821, 1991
; Tritle: Functional duality and structural uniqueness of depressant insect-selective neu
; Reference umber: A38526; MUID:91230120; PMID:2029523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Primary structure of scorpion anti-insect toxins isolated from the venom of Lei
Reference number: S08267; MUID:90184494; PMID:2311768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
     ä
                                                                                                                                                                                                                           depressant insect toxin LqqIT2 - scorpion (Leiurus quinquestriatus)
C;Species: Leiurus quinquestriatus
C;Species: Leiurus quinquestriatus
C;Date: 06-Jul.1990 #sequence revision 06-Jul.1990 #text_change 09-Jul-2004
C;Accession: B34123; S08268; B38526
R;Zlotkin, E; Fowler, E.; Eitan, M.; Moyer, M.; Adams, M.E.
Toxicon 28, 170, 1990
A;Title: On the chemistry and action of the depressant insect toxins.
     Gaps
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     Indels
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F;10-60,14-35,21-42,25-44/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1566,'S',1568-3133 <MOR>
A;Cross-references: EMBL:D29738; NID:9474967; PID:9664884
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 2
Pred. No. 0.73;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: P98092; EMBL: D29738
  3; Mismatches
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A;Reference number: S70920
                                                                                                   79 ECSALCOMDGECPETOKCCSSGCSROC 105
                                                 ECESICGADGAC -- - WTWCADGCSRSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNKECKSYGGSYGYCWTW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CIRECESICGADGACWTW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: CAS:130300-67-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: scorpion neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Reference number: A34123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-3133 <KOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: protein
Residues: 1-61 <ZLO2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S08268
     12;
  Matches
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depressant insect toxin LghIT2 precursor - scorpion (Leiurus quinquestriatus)
C;Species: Leiurus quinquestriatus hebraeus
C;Date: 21-Jul-1995 #sequence revision 28-Jul-1995 #text_change 09-Jul-2004
C;Accession: A61616; A34123; Ā38526
C;Accession: A61616; A34123; Ā38526
Insect Biochem. Nol. Biol. 22, 199-203, 1992
A;Title: Molecular analysis of cDNA and the transcript encoding the depressant insect sel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A;Residues: 22-82 -22.02.01.
R;Zlotkin, E.; Eitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhart, W.; Fowler, I
Biochemistry 30, 4814-4821, 1991
A;Title: Punctional duality and structural uniqueness of depressant insect-selective neum
A;Reference number: A38526; MUID:91230120; PMID:2029523
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A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:O17970; EMBL:Z81573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M02
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 22-82 < ZLC2>
A; Cross-references: CAS:130300-64-0
C; Superfamily: scorpion neurotoxin
C; Superfamily: scorpion neurotoxin
C; Superfamily: scorpion eurotoxin
P;1-11/Domain: signal sequence #status predicted < SIG>
P;12-21/Domain: propeptide #status predicted < RIG>
P;22-82/Product: depressant insect Coxin LqHIT2 #status experimental < MAT>
P;31-81,35-56,42-63,46-65/Disulfide bonds: #status predicted
P;82/Modified site: amidated carboxyl end (Gly) (amide in mature form from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                        Gaps
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R;Zlotkin, B.; Fowler, E.; Eitan, M.; Moyer, M.; Adams, M.E.
Toxicon 28, 170, 1990
A;Title: On the chemistry and action of the depressant insect toxins.
A;Reference number: A34123
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Length 3133;
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Pred. No. 1.9;
4; Mismatches 5; Indels
DB 2;
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A;Residues: 1-85 <ZIL>
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                                                                                                                                                                                       2 YNLCIRECESICGADGACWTWCADGCSRSC 31
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hypothetical protein F42F12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22100
A;Holyd, C.
submitted to the EMBL Data Library, November 1995
A;Reference number: 219514
A;Accession: T22100
A;Accession: T22100
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T2210
A;Accession: 1-163 - WIA-
A;Residues: 1-163 - WIA-
A;Residues: 1-163 - WIA-
A;Residues: 1-163 - WIA-
A;Experimental source: clone F42F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rilloyd, C.
submitted to the EMBL Data Library, November 1995
A;Reference number: 219514
A;Accession: T22102
A;Accession: T22102
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-164 - WIL>
A;Residues: 1-164 - WIL>
A;Residues: UNIPROT: Q20345; EMBL: Z68116; PIDN: CAA92174.1; GSPDB: GN00028; CESP: F42;
A;Experimental source: clone F42F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A21761
high-cysteine chorion A 12 protein precursor - silkworm
high-cysteine chorion A 12 protein precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Species: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 26-Aug-1999
C;Date: 20-Jul-1990
C;Date: 20-Jul-199
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22102
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2
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C;Superfamily: Caenorhabditis elegans hypothetical protein F42F12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ů
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 31.6%; Score 62.5; DB 2; Length 163; al Similarity 41.9%; Pred. No. 4.4; 13; Conservative 4; Mismatches 9; Indels
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Best Local Similarity 41.9%; Pred. No. 4.4;
Matches 13; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 CYNLCVHNCAAV--YDGSCTT---DPDFRCC 140
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A,Molecule type: DNA
A,Residues: 1-124 <IAT>
C,Superfamily: chorion class A protein pc292
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A;Reference number: 219781
A;Accession: T23682
A;Accession: T23682
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-294 <MIL>
A;Residues: 1-294 <MIL>
A;Residues: 1-294 <MIL>
A;Residues: 1-204 <MIL>
C;Genetics: UNIPROT:Q9XUSO; EMBL:281573; PIDN:CAB04626.1; GSPDB:GN00020; CESP:MC
C;Genetics:
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A,Molecule type: DNA
A,Residues: 1-163 <WIL>
A,Cross-references: UNIPROT:Q20342; EMBL:Z68116; PIDN:CAA92171.1; GSPDB:GN00028; CESP:F4
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                         A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
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                                                                                                                                      Query Match 32.3%; Score 64; DB 2; Length 1513; Best Local Similarity 35.5%; Pred. No. 14; Matches 11; Conservative 2; Mismatches 18; Indels
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A;Reference number: 219514
A;Accession: T22099
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                                                                                                                                                                                                                                                                                                                 1 CYNLCIRECESICGADGACWIWCADGCSRSC 31
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A;Introns: 20/3; 76/2; 182/3; 223/3
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A,Gene: CESP:F42F12.7
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T22100
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Query Match
Best Local Similarity
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A;Introns: 30/3; 296/2
C;Superfamily: gliadin
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A;Gene: CESP:ZK1067.7
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A;Nolecule type: DNA
A;Nolecule type: Larace translated from GB/EMBL/DDBJ
A;Residues: 1-372 < WILD-
A;Cross-references: UNIPROT:017969; EMBL:Z81573; PIDN:CAB04624.1; GSPDB:GN00020; CESP:MC
A;Experimental source: clone M0269
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A;Cross-references: UNIPROT:Q19182; EMBL:Z68314; PIDN:CAA92662.1; GSPDB:GN00020; CESP:FG
A;Experimental source: clone F07H5
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23G80
R;Matthews, L.
                                                                                                                                                                                                                                           hypothetical protein F07H5.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20561
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                                               11;
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Query Match 31.1%; Score 61.5; DB 2; Length 124; Best Local Similarity 31.0%; Pred. No. 4.7; Matches 13; Conservative 2; Mismatches 16; Indels 11
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Pred. No. 15;
4; Mismatches 16; Indels
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                                                                                         1 CYNLCIRECESICGADGACWTWCAD------GCSRSC 31
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A;Introns: 17/3; 72/3; 181/3; 232/2; 258/3; 294/3; 336/1
C;Superfamily: gliadin
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                                                                                                                                                                                                                                                                                                                                            R;Steward, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19292
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A;Introns: 32/3; 81/3; 489/3; 591/3; 633/3
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30.3%;
Best Local Similarity 31.4%;
Matches 11; Conservative 4
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les 11; Conserv
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hypothetical protein ZK1067.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

RESULT 14

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A;Residues: 1-314 <WIL>
A;Cross-references: UNIPROT:Q23390; EMBL:Z70038; PIDN:CAA93886.1; GSPDB:GN00020; CESP:ZKJ
A;Experimental source: clone ZK1067
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C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52415
R;Bilodeau, P.; Luo, M.; Dennis, E.S.; Peacock, W.J.; Chaudhury, A.M.
A;Reference number: 226069
A;Accession: T52415
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T27686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.1%; Score 59.5; DB 2; Length 856; Best Local Similarity 46.4%; Pred. No. 29; Matches 13; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.1%; Score 59.5; DB 2; 29.0%; Pred. No. 15; tive 7; Mismatches 14;
                                                        Rithomas, K. submitted to the EMBL Data Library, March 1996 A; Reference number: 220404 A; Accession: T27686 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-856 <BIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CIPVCLAQCQSSC-QTSQCIQQCQPACNQQC 90
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Q20345 caenorhabdi Q814j0 caenorhabdi Q814j1 caenorhabdi Q814j1 caenorhabdi Q810243 caenorhabdi Q81025 mus musculu Q811g8 mus musculu Q71ng6 mus musculu Q71ng6 mus musculu Q71c30 giardia lam Q61s34 mus musculu Aah65956 mus musculu Q81ck8 mus musculu Q81ck8 mus musculu Q81ck8 mus musculu

Sequence:

Run on:

Searched:

Database

Result

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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              017982 PRELIMINARY, PRT; 572 AA.
017982, 017986 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Prion-like-(Q/n-rich)-domain-bearing protein 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                          WFD3 HUMAN
QBR1G8
QBR1H9
Q7TNG6
Q7R630
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AAH69956
Q20345
Q814J0
Q814J1
Q8WQG6
Q20343
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QBKOP6
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R.;
Submitted (JUN-2004) to the EMBI
EMBL, 013141; AAA96110.3; -.
PIR; T30136; T30136.
HSSP, P56679; 1PBI.
WormPep; C14C11.8; CE27684.
InterPro; IPR003341; DUF139.
InterPro; IPR006209; EGF_like.
Pfam; PP02363; C_tripleX; 15.
PROSITE; PS01186; EGF_2; 1.
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Caenorhabditis elegans.
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STRAIN=Bristol N2;
Du Z., Gattung S.;
Submitted (APR-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
Submitted (NOV-2002)
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Best Local Similarity
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STRAIN=Bristol N2;
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NCBI_TaxID=6239;
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SEQUENCE
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Q17982
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Cabd4551 caenorhab
Cae4650 caenorhab
Cae4650 caenorhab
O8440 coryca sativ
O8146 coryca sativ
O8116 coryca sativ
P19855 leiurus qui
P98052 bombyx mori
P92716 arabidopsis
Q8brc8 mus musculu
Q7unp4 rhodopirell
Q5npQ4 drosophila
Q9cqv drosophila
Q9cqv drosophila
Q9cqv drosophila
Q8659 drosophila
Q8659 drosophila
Q8659 drosophila
Q86620 drosophila
Q86630 drosophila
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225904 buthus occi
22592 leiurus qui
017970 caenorhabdi
28ilm9 plasmodium
9xus0 caenorhabdi
22347 drosophila
023948 drosophila
023948 caenorhabdi
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                                                                                                                                                                           ; ; Search time 184.83 Seconds (without alignments) 96.503 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1825181
                            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1825181 segs, 575374646 residues
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LCR1_ARATH
Q8BRC8
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Maximum Match 100%
Listing first 45 summaries
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CAB04551
CAE48500
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    protein search, using sw model

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Q6NP04
AAR82794
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Q9XUS0
Q23947
Q23948
Q20342
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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                                                                                                                               OM protein
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Maximum DB
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Length 572;

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Name=kal-1;
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                           Bugarli E.T., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF34296f; AAL7338.1; -.

InterPro; IPR003961; FN III.

InterPro; IPR008957; FN III.-like.

InterPro; IPR008197; WAP.

Ffam; PP00041; fn3; 3.

Pfam; PP00005; WAP; 1.

PRINTS; PR00006; FN3; 3.

SMART; SM00017; WAP 1.

PROSITE; PS00317; WAP 1.

PROSITE; PS00317; WAP 1.

PROSITE; PS00317; WAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.1%; Score 69.5; DB 2; Length 700; 44.4%; Pred. No. 3.7; tive 3; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.1%; Score 69.5; DB 2; Length 700; Best Local Similarity 44.4%; Pred. No. 3.7; Matches 12; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
C. elegans KAL-1 protein (Corresponding sequence K03D10.1).
KAL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White S.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81561; CAB04551.2; -.
EMBL; Z92828; CAB04551.2; JOINED.
SEQUENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             78584 MW; 2975913064E981E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             700 AA.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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CAB04551;
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CAE48500
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  ö
  Gaps
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                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
  14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00317; 4 DISULPIDE_CORE; 1.
PROSITE; PS50853; FN3; 2.
Hypothetical_protein.
SEQUENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;
                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein K03D10.1.
Name=K03D10.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                 452 CVQACQPQCQQTCGSNVQCVSACQNSCQQSC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           700 AA
7; Mismatches
                                       1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                                                            700 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 ECESICGADGAC --- WIWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z81561; CAB04551.2; ...
EMBL; Z92828; CAB04551.2; JOINED.
EMBL; ESTS61, CAB04551.2; JOINED.
EMBL; Z92828; CAE48500.1; JOINED.
EMBL; T23271; T23271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WormPep; K03D10.1; CE18005.
InterPro; IPR003361; FN III.
InterPro; IPR008957; FN III-like.
InterPro; IPR008197; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00060; FN3; 3.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 20, (TrEMBLrel. 20, I
  10; Conservative
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                                                                                                                                                                                          PRELIMINARY;
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Pfam, PF00041; fn3; 3.
Pfam, PF00095; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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01-MAR-2002 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White S.;
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Q8WS94;
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08WS94
ID 08WS
AC 08WS
DT 01-M
DT 01-M
Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A POLYCOMB group gene of rice (Oryza sativa L. subspecies indica), OsiEZ1, codes for a nuclear-localized protein expressed preferentially in young seedlings and during reproductive development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22890056; PubMed=14527713;
Thakur J.K., Malik M., Bhatt V., Reddy M.K., Sopory S.K., Tyagi A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Lillopsida; Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.1%; Score 67.5; DB 1; Length 895; 42.9%; Pred. No. 8.1; ive 4; Mismatches 9; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 78 Poly-Ala.
895 AA; 100392 MW; 2659DCF992A08919 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647 YNPCV--CQQMCGKDCPCVENGTCCEKYCGCSKSC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC 31
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SMART; SM0017; SANT; 1.
SMART; SM01317; SET; 1.
PROSITE; PS00117; 4 DISULFIDE_CORE; UNKNOWN_1.
PROSITE; PS50280; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene family; Nuclear protein; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             895 AA
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001005, Myb_DNA_binding.
InterPro; IPR001214; SET.
Pfam; PF00856; SET; 1.
SMART; SM00717; SANT; 1.
SWART; SM00317; SET; 1.
PROSITE; PS50090; WYB 3; FALSE_NEG.
PROSITE; PS50280; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SET.
Cys-rich.
SIMILARITY: Contains 1 SET domain.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001005; Myb_DNA_binding.
InterPro; IPR001214; SET.
InterPro; IPR008197; WAP.
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                                                                                                                                                                                                                                                                                                                                          EMBL; AF443598; AAM13422.1; -.
MaizeDB; 754846; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enhancer of zeste protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Franscription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 314:1-13(2003)
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Matches
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Q84UI6
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**Springer N.M., Danilevskaya O.N., Hermon P., Helentjaris T.G., Phillips R.L., Kaeppler H.F., Kaeppler S.M.;

**Sequence relationships, conserved domains, and expression patterns are the mologis of the Polycomb group genes E(z), esc, and E(PC).";

**Purile Physiol. 128:1332-1345(2002).

**Purile Physiol. 128:134:1345(2002).

**Purile Physiol. 128:134:1345(
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Rhabditidae; Peloderinae; Caenorhabditis.
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                       -MAR-2004 (TrEMBLrel. 27, Last sequence update)
-MAR-2004 (TrEMBLrel. 27, Last annotation update)
elegans KAL-1 protein (Corresponding sequence K03D10.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Seed;
MEDLINE=21948211; PubMed=11950982; DOI=10.1104/pp.010742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White S.; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2004). .. EMBL, 292818; CAE48500.1; JOINED. EMBL, Z81561; CAE48500.1; JOINED. CEPTINGE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-Jycomb protein E23 (Enhancer of zeste protein 3)
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700 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 ECSALCOMDGECPETOKCCSSGCSRQC 143
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                                                                   02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last seq
02-WAR-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=EZ3; Synonyms=MEZ3;
Zea mays (Maize).
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                                                                                                                                                                                                                                          Caenorhabditis elegans.
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Matches 12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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MEDLINE=22357239; PubMed=12467668;
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                                                                                                        SEQUENCE OF 22-82.
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzase, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zou C.,
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            Score 67.5; DB 2; Length 895;
Pred. No. 8.1;
3; Mismatches 9; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.1%; Score 67.5; DB 2; Length 895; 45.7%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22751709; PubMed=12815033;
Liang Y.-K., Wang Y., Zhang Y., Li S.-G., Lu X.-C., Li H.,
X. Z.-H., Bai S.-N.;
"OSSET!, a novel SET-domain-containing gene from rice.";
J. Exp. Bot. 54:1995-1996(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liang Y., Bai S., Xu Z.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407010; AAN01115.1; -.
HSSP; P10968; 7WGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99800 MW; 47AA0F5DBFB7C84F CRC64;
                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grameno; 081LD6; -
Go; 60:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005637; F:DNA binding; IEA.
InterPro; IPR001204; SET.
InterPro; IPR008197; WAP.
InterPro; IPR008197; WAP.
SWART; SW00317; SET; 1.
SWART; SW00317; SET; 1.
PROSITE; PS00317; A INSULFIDE CORE; UNKNOWN 1.
PROSITE; PS00317; A INSULFIDE CORE; UNKNOWN 1.
SEQUENCE 895 AA; 99800 MW; 47AAOF5DBFB7C84F C3
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            un 34.1%;
I Similarity 45.7%;
16; Conservative
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            Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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SIX2_LEIQU
JD 21X2_LEIDU
DT 29-MAR
DT 05-JUL
DS Leiuru
OC Eukary
OC Buthid
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Zaki T.I., Maruniak J.E.;
"Three polymorphic genes encoding a depressant toxin from the Egyptian scorpion Leiurus quinquestriatus quinquestriatus.";
Toxicon 41:109-113(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90184494; PubMed=2311768;
Kopeyan C., Mansuelle P., Sampieri F., Brando T., Bahraoui E.M.,
Rochat H., Granier C.;
"Primary structure of scorpion anti-insect toxins isolated from the
venom of Leiurus quinquestriatus quinquestriatus.";
FEBS Lett. 261:423-426(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Venom;
MEDLINE-91230120; PubMed=2029523;
Zlotkin E., Eiten M., Bindokas V.P., Adams M.E., Moyer M.,
Burkhart W., Fowler E.;
"Functional duality and structural uniqueness of depressant insect-selective neurocoxins.";
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Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
Polymorphism; Signal; Sodium channel inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93160530; PubMed=8431601;
Zlotkin E., Gurevitz M., Fowler E., Adams M.E.;
"Depressant insect selective neurotoxins from scorpion venom:
Chemistry, action, and gene cloning.";
Arch. Insect Biochem. Physiol. 22:55-73(1993).
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HSSP; P01494; 2SN3.
InterPro; IPR002061; Scorpion_toxinL.
Pfam; PF00537; Toxin 3; 1.
PRINTS; PR00285; SCORPNTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lochemistry 30:4814-4821(1991).
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EMBL; AF474985; AAM74029.1; -.
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                                                                                                                                                                                                                                         Hemocytin precursor (Humoral lectin).
Bombyx, mori (Silk moth).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                STRAIN=Fuyou X Tokai; TISSUE-Hemocyte;
MEDLINE=95178544; PubMed=7873598;
Kotani E., Yamakawa M., Iwamoto S.-I., Tashiro M., Mori H., Sumida M., Matsubara F., Taniai K., Kadono-Okuda K., Kato Y., Mori H.;
McIoning and expression of the gene of hemocytin, an insect humoral lectin which is homologous with the mammalian von Willebrand factor.";
Biochim. Biophys. Acta 1260:245-258(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteolysis.
--- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
--- SIMILARITY: Contains 2 F5/8 type C domains.
--- SIMILARITY: Contains 2 VWFC domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2221-3133 FROM N.A.
Kotani E., Iwamoto S.I., Tashiro M., Mori H., Sumida M., Matsubara
Yamakawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- INDUCTION: Hemagglutination activity is increased by bacterial viral infection and inhibited by D-mannose, N-acetyl-D-galactosamine and D-maltose.
-!- PTM: May be converted into the 260 kDa mature hemocytin by
                                                                               ö
                                                       Score 67; DB 1; Length 82;
Pred. No. 1.1;
3; Mismatches 5; Indels
N -> D.
S -> A.
D -> E.
F13D53B18CDECBF0 CRC64;
                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                   PRT; 3133 AA
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EWBL; D14035; BAA03124.1; -...
FIR; S25093; S52093.
HSSP; P00451; 110D.
INTERPC; IPR002019; Cysrich TIL.
INTERPC; IPR00421; Cysrich TIL.
INTERPC; IPR00421; FASS C.
INTERPC; IPR00941; PASS C.
INTERPC; IPR00941; PWP_C.
INTERPC; IPR001041; PWP_C.
INTERPC; IPR001044; WWP_C.
                                                                                                   5 CIRECESICGADGACWTW 22
                                                                                                                 CNKECKSYGGSYGYCWTW 59
43 43 1
48 48
71 71 1
82 AA; 9099 MW; 1
                                                     33.8%;
                                                                              10; Conservative
                                                                                                                                                                                  STANDARD;
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NCBI TaxID=7091;
                                                                    Local Similarity
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                                                        Query Match
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R Pfam; PF00754; F5 F8 LYPe_C; 2.

R Pfam; PF01826; TIE; 6.

R Pfam; PF00184; VWD; 3.

R PROSITE; PS01225; CTCK 1; 1.

R PROSITE; PS01225; CTCK 2; 1.

R PROSITE; PS01286; PA58C 1; 2.

R PROSITE; PS01286; PA58C 2; 2.

R PROSITE; PS01286; VWFC 1; PALES NEG.

Cella adhesion; Glycoprotein; Lectin; Repeat; Signal.

SIGNAL

I DOWAIN 153 240 D'.

I DOWAIN 1283 1356 D'.

I DOWAIN 150 1951 DJ.

I DOWAIN 15230 2321 C-TYPE LECTIN (ATYPICAL).

R DOWAIN 2330 2321 C-TYPE LECTIN (ATYPICAL).
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RESULT 11

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RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Rahakida K., Indtani Y., Ishii Y., Itch M., Kagawa T., Kasiwa T., Kasimi Y., Indiani Y., Konho S., Konno H., Kowda M., Koya S., RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kowda M., Roya Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Rasaki C., Saitoh H., Saato R., Santo R., Saitoh H., Sakai C., Sakazue N., Gazaki Y., RA Saaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tagami H., Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.

R. BMBL, AKO45114, BAC32228.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
  Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
enriched library, clone:B130034E13 product:hypothetical protein, full
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;

MEDLINE=20350913; PubMed=11076861;

MEDLINE=20350913; PubMed=11076861;

Schibate K., Itoh M., Akiyawa K., Nishia T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional amotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                STRAIN-C57BL/65; TISSUB-Parthenogenote;
MEDLINE-9927253; PubMed-10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Parthenogenote;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUB=Parthenogenote;
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                                                                     musculus (Mouse).
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Best Local Similarity
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                                                                                                                                    NCBI_TaxID=10090;
                                              insert sequence
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21330246; PubMed=11437247; DOI=10.1023/A:1010664704926; Vancosthnyse V., Miege C., Dumas C., Cock J.M.;
"Two large Arabidopsis thaliana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and the male component of the self-incompatibility response."; Plant Mol. Biol. 46:17-34(2001).
-!- TISSUE SPECIFICITY: Expressed in flower buds, but not in stems, roots or rosette leaves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequel features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Low-molecular-weight cysteine-rich protein LCR1.
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                                                                                                                                                                                                                          05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Low-molecular-weight cysteine-rich protein LCR1 precursor.
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Last annotation update)
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                                                                                                                                                             89 AA
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YNLCIRECESICGADGACWTWCADGCSRSC
                         31 YN--VKECELSC-TGGQQYTVCADSCLRKC
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InterPro; IPR010851; SLR1-BP.
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(TrEMBLrel. 23, I
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                                                                                                                                                           STANDARD;
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SIGNAL

Matches

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Q8BRC8

RESULT 12 Q8BRC8 ID Q8BRC AC Q8BRC DT 01-MA DT 01-MA

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591 AA; 64870 MW; D08400487404CFE8 CRC64;
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                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR002223; Prot Inh_Kunz-m.
InterPro; IPR008197; WAP.
Fam; PF00047; ig; 3.
Fam; PF00004; Kunitz_BPTI; 1.
Pfam; PF000095; WAP; 1.
                                                                                                                                                                                                                                                                                                   PRINTS; PRO003; 4DISULPHCORE.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Prot_Inh_Kunz-m; 1.
SMART; SM00409; IG; 3.
SMART; SM00408; IGc2; 3.
SMART; SM00131; KU; 1.
SMART; SM00131; KU; 1.
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PROSITE; PS00022; EGF_1; U
PROSITE; PS50835; IG_LIKE;
PROSITE; PS50900; PLAC; 1.
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SEQUENCE
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungalz C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula
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Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales, Planctomycetaceae, Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.8%; Score 65; DB 2; Length 838; 46.2%; Pred. No. 15;
Indels
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-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; BT011127; AAR82794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF07639; YTV; 5.
PROSITE; PS01039; 4FEAS FERREDOXIN; UNKNOWN 1.
Complete proceme; Hypothetical protein.
SEQUENCE 838 AA; 92235 MW; 84AD168706763544 CRC64;
                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
BmBL; BX29446; CAD75374.1; -.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR011521; YTV.
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches 13;
                                                          1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                 10 CVCVCVCVCVCVCARACDRYCSHACARYC 40
                                                                                                                                                                                                                                                                                   838 AA
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.8
Best Local Similarity 46.2
Matches 12; Conservative
10; Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
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Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Clampe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 32.6%; Score 64.5; DB 2; Length 591; Local Similarity 41.4%; Pred. No. 13; Nonservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases EMBL; BT011127; AAR82794.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591 AA; 64870 MW; D08400487404CFE8 CRC64;
                                                  02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
LD02520p (Fragment).
591 AA
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Job time : 186.83 secs

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; Search time 51.283 Seconds (without alignments) 62.956 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                               November 16, 2004, 14:09:48
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

	non	Selective	Aminopept		-		•	-	Human pol	Human	Human	Breast	Breast ca	Breast tu	Integrin-	•	Human bre	Human bre	Integrin-		٠.	_	CH1 delet	Human gen		_
	Description	Abg60448	Abr56860	Abg60452	Abr 56864	Abg60450	Abr56862	Aag74702	Aam38740	Abg70171	Aam40526	Aaw13427	Aaw60290	Aaw93627	Aab17959	Aab17923	Aab21702	Aae06280	Aau81104	Abb72956	Adj73110	Adj52745	Adj51706	Aae03911	Abb57419	Ada98407
SUMMARIES		148	160	152	164	150	162	702	140	.71	126	127	06;	.27	59	123	.02	180	.04	56	10	45	90	11	19	0.2
-	a :	ABG6044	ABR56860	ABG60452	ABR56864	ABG60450	ABR5686	AAG7470	AAM3874	ABG70171	AAM40526	AAW13427	AAW60290	AAW93627	AAB17959	AAB17923	AAB21702	AAE06280	AAU81104	ABB72956	ADJ73110	ADJ52745	ADJ51706	AAE03911	ABB5741	ADA98407
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	Score	57	57	20	20	47	47	44	43	43	43	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40
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Ada98405 Human sec Ada98404 Human sec Ada98396 Human sec Ada44203 Human sec Ada44203 Human sec Ada44202 Human sec Ada44202 Human sec Adc20563 Human sec Adc20563 Human sec Adc20579 Human sec Adc20579 Human sec Adc20578 Human sec	Human Human Human Human Human Human
43 6 ADA98405 43 6 ADA98404 43 6 ADA98396 43 6 ADA44191 43 6 ADA44205 43 6 ADA44205 43 7 ADC20563 43 7 ADC20573 43 7 ADC20578	43 7 ADF10801 43 7 ADF10805 43 7 ADF10805 44 4 AAU01745 44 4 AAU01069 44 4 AAU01069 44 4 AAU01069 44 4 AAU01949 63 7 ADF11750
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## ALIGNMENTS

Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic; Selective targeting peptide #123. ABG60448 standard; peptide; 9 AA. (first entry) gene therapy. 30-JUL-2002 ABG60448; 

Synthetic.

WO200220769-A1.

14-MAR-2002.

07-SEP-2001; 2001WO-US027692

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.

(TEXA ) UNIV TEXAS SYSTEM.

Pasqualini R; Arap W, WPI; 2002-415731/44

Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular disease.

Claim 22; Page 102; 317pp; English.

The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with ischaemia, cancer, arthritis, diabetes, cardiovascular disease,

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Indels

Length 9;

100.0%; Score 57; DB 6; I 100.0%; Pred. No. 1.7e+06;

Mismatches

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Conservative

Local Similarity

Best Loc Matches

Query Match

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Gaps

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the
attaching
inflammation or macular degeneration. Furthermore, the peptide is useful
                                                                                                                                                                                                                                                                                                                                                      Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...catlug opesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to subject.
         for diagnosing the diseases cited above. Targeting perides of the invention can also be used to deliver an agent to a foetus, by atta a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60326-ABG60574 represent selective targeting peptides of the invention
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                                                                                                                                      Indels
                                                                                                              Length
                                                                                                                                                                                                                                                                                                                               Aminopeptidase A (APA) binding peptide SEQ ID NO:56.
                                                                                                             100.0%; Score 57; DB 5; L
100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 98; 247pp; English.
                                                                                                                                                                                                                                                      ABR56860 standard, peptide; 9 AA.
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                                                                                                                           100.08;
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                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                       Conservative
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                                                                                                                                                                                         CPRECESIC 9
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                                                                                                             Query Match
Best Local Similarity
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                                                                                      Sequence 9 AA;
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                                                                                                                                                 Targeting peptide, cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antiidabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 22; Page 109; 317pp; English
               ABG60452 standard; peptide; 13 AA.
                                                                                                                   Selective targeting peptide #127.
                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEXA ) UNIV TEXAS SYSTEM.
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 88.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arap W, Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPRECESNC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
                                                                                                                                                                                                                                                                                                        WO200220769-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides of
                                                                                  30-JUL-2002
                                                                                                                                                                                                                                                                                                                                         14-MAR-2002.
                                                                                                                                                                                                                                                                        Synthetic.
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Matches
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ABG60452
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The present invention describes a method for treating obesity or a selective for adipose tissue; (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and dispose targeting peptides have anorectic and antilipaemic activities, and can be used in peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immundeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for tearappenic activity. ABRS6806 to ABRS6827 and ACC79106 to ACC79111 represent sequences used in the exemplification of the present invention

Sequence 9 AA;

Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101. 07-SEP-2001; 2001WO-US027692

WO200220769-A1

14-MAR-2002

gene therapy.

Synthetic.

(TEXA ) UNIV TEXAS SYSTEM.

WPI; 2002-415731/44. Arap W, Pasqualini

Selective targeting peptide #125.

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The present invention describes a method for treating obesity or a lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and (d) inducing weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teratogenic activity. ABR56806 to ABR56827, and ACC79106 to ACC79111 represent sequences used in the
                                                                                                                                                                                                                 peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to subject.
                                                                                                                                                                                                 antilipaemic;
                                                                                                                                                                                             Targeting peptide; obesity; lipodystropathy; anorectic;
                                                                                                                                                         Aminopeptidase A (APA) binding peptide SEQ ID NO:60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 104; 247pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kolonin MG;
                                       ABR56864 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-2002; 2002WO-US027836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001; 2001WO-US027692.
                                                                                                                     30-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasqualini R, Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-371749/35.
                                                                                                                                                                                                                                                                                                                                    WO2003022991-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2003.
                                                                                                                                                                                                                                                                                               Synthetic
                                                                               ABR56864;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, eg. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, varial infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with inflammation or macular degeneration. Furthermore, the peptide is useful for diagnosing the disease cited above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60326-ABG60574 represent selective targeting
                                                                                                                                                                                                                                                                                                                                                                                                       Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Targeting peptide, obesity, lipodystropathy, anorectic, antilipaemic, peptide therapy, gene therapy, infection, human immunodeficiency virus, HIV, placental delivery, teratogenic, placenta, adipose, pancreatic, beta-1 integrin, beta-5 integrin, spleen, aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aminopeptidase A (APA) binding peptide SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 9
Pred. No. 6.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 108; 317pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR56862 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease.
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Gaps ö

DB 6; Length 13; 1; Indels

Score 50; DB 6 Pred. No. 1.1; 0; Mismatches

87.78; 88.98;

8; Conservative

Best Local Similarity Matches 8; Conserv

Query Match

CPRECESNC 13 CPRECESIC 9

ઠ 요 ABG60450 standard; peptide; 31 AA.

RESULT 5 ABG60450 (first entry)

30-JUL-2002

ABG60450;

SXXXE

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The present invention describes a method for treating obesity or a lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and (d) inducing weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in the subject or treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for treatogenic activity. ABN55816 to ABN55927 and ACC79101 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                  Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 6; Length 31;
Pred. No. 6.3;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer antigen protein SEQ ID NO:5466.
                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 104; 247pp; English
                                                                                                                                                                                                        Kolonin MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG74702 standard; protein; 58 AA.
                                                                                                            30-AUG-2002; 2002WO-US027836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.5%;
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                                                                                                                                           07-SEP-2001; 2001WO-US027692
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Best Local Similarity 88.3.,
Best Local Similarity 88.3.
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                                                                                                                                                                         (TEXA ) UNIV TEXAS SYSTEM
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                                                                                                                                                                                                                                       WPI; 2003-371749/35.
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                                              WO2003022991-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31 AA;
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03-NOV-1999;
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                                                                             20-MAR-2003
                Synthetic.
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cancer-associated mucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have gyrostatic activity and can be used in gene therapy and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, nootropic, immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                 AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                  Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB Pred. No. 29; 1; Mismatches
                                                                                                                                                                               Claim 11; Page 7070-7071; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM38740 standard; protein; 460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 1885.
                                                  Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00471275.
2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2000; 2000WO-US034263
                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 CPRECSFLC 37
                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                  2001-235357/24
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                                                                                                N-PSDB; AAH34107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia.
                                                  Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM38740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Wang D; , Zhao QA;

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encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polymetide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chaence system suppression, Activin/inhibin activity, chaencetic/chemokinetic activity, haemostatic assays for receptor activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; selected interacting domain; human.
                                                                                                                                                                                                                        nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                             Ren F, Wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 4; Length 460;
Pred. No. 2.3e+02;
3; Mismatches 1; Indels
                                                                                                           Qian XB,
Yang Y,
                                                                                                         Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                       Example 3; SEQ ID NO 1885; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prey protein for Shigella ipaH9.8 #1.
                                                                                                                                                                                                                                        as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG70171 standard; protein; 501 AA
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00665191.
19-OCT-2000; 2000US-0053036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.4%;
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                                                                                                                                                                         2001-442253/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                         N-PSDB; AAI57896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200257303-A2.
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                                                                                                         YT,
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ص
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                        Novel
                                                                                                              Tang
                                                                                                                               Wang
                                                                                                                                             Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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The invention relates to a complex of protein-protein interactions between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaD, ipaC, ipaH9.8 w. ospG and ospC1) and a mammalian polypeptide defined in the specification. The complexes are formed using the yeast two-hybrid system. Also included are (1) a recombinant host cell expressing the interactions between the Shigella flexneri polypeptide and a mammalian polypeptide and a mammalian polypeptide defined in the specification; (2) selecting a modulating compound that inhibits or activates the protein-protein interactions; (3) a modulating compound obtained from the method of (2); (4) a SID (comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a SID polypeptides a vector comprising the vording the comprising the vector; and (10) a protein chip comprising Shigella containing the vector; and (10) a protein chip comprising Shigella (lexancin polypeptide or polymucleotide is useful for treating or preventing special composition comprising the present comprising the composition of polypeptide or polymucleotide is useful for treating or preventing and a mammalian polypeptide or mammal. The present containing the polymucleotide is useful for mammal. The present containing the present composition comprising the present containing the present composition and mammal the present containing the present composition and mammal the present containing the properties and a mammal containing the composition and containing the present containing the present containing the properties and containing the properties and containing the present containing the properties and containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents a human prey protein isolated by the yeast two-hybrid
                                                                                                                    flexneri polypeptide and a prey mammalian or human placenta polypeptide
for treating or preventing bacillary dysentery in a mammal or human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, nootropic, immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroslis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                               New complex of protein-protein interactions between a bait Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assay, forming a complex of the invention with a shigella protein
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                  Claim 7; Page 116-117; 162pp; English.
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2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00698042.
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87.5%;
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                         WPI; 2002-599706/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRECESIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                              N-PSDB; ABS51564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 501 AA;
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20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1999;
21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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This synthetic peptide is a claimed example of a breast tumour-homing peptide that was identified using a novel method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method trypically involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see AAM1181-52, AAW1181-86) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour homing molecules and their conjugates - useful for, e g. directing linked moiety to tumour containing angiogenic vasculature.
                                        Obtaining compound that homes to selected organ or tissue - by in vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour homing peptide; in vivo panning; breast carcinoma; alpha-V-containing integrin binding motif; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2; Length 13;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breast carcinoma tumour homing peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 6; 105pp; English.
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                                                                                                                          Claim 18; Page 68; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW60290 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US016086
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                                                                                                                                                                                                                                                                                                                                                                                                 maintain specificity in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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    WPI; 1997-202359/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPRECESIC
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9810795-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW60290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW60290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic acitvity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system disease, such as localised neuropathies and central nervous system disease, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosts, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                            Ren F, Wang D;
Zhang J, Zhao QA;
                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breast tumour homing peptide; cancer; in vivo panning; screening; phage display; drug delivery.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                       Liu C, Asundi V, Chen R, Ma Y, Qian XB, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.4%; Score 43; DB 4; L
55.6%; Pred. No. 2.5e+02;
ive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 5457; 10078pp; English.
                                                                                                                                                                                                                                                                                            as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW13427 standard; peptide; 13 AA.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t Local Similarity 55.6
ches 5; Conservative
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                                                                                                                                                                                                           WPI; 2001-442253/47.
                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                            N-PSDB; AAI59682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 512 AA;
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                                                                                                                                                 Wang J,
Zhou P,
                                                                                                                     rang YT,
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The present peptide represents a tumour homing peptide, and is produced by in vivo panning. The peptide homes to a breat carcinoma. The in vivo panning comprises administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying a peptide that homes to the tumour, collecting a sample of normal tissue corresponding to the tumour, and determining that the peptide that homes to the tumour is not present in the normal tissue. The tumour homing

(LJOL-) LA JOLLA CANCER RES FOUND.

Pasqualini R;

Ruoslahti E,

95US-00526710

95US-00526708

11-SEP-1995;

RESULT 11 AAW13427

Matches

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11-SEP-1995;

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Gaps ;

Indels

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inflammatory, anti-angiogenic and anti-arthritic activity. Such molecules are identified by treating a purified NGR receptor with a test compound and identifying compounds that bind specifically to the NGR receptor. The peptides of the invention are inhibitors of angiogenesis and can be used to produce conjugates for delivering agents to angiogenesis and can be used by treaticularly anticancer drugs or an imaging agents to angiogenic vasculature, particularly anticancer drugs or an imaging agent, for diagnosis or prognosis. These conjugates may be directed to non-tumour angiogenic vasculature, e.g. that present in inflammatory, regenerating or wounded tissue, e.g. for treatment of macular degenerating, diabetic retinopathy or rheumatoid arthritis. The peptides provide specific targeting to rumours, especially their supporting vasculature, since the NGR receptor is exposed to the circulation only in angiogenic vasculature. Precise targeting should reduce the systemic toxicity of anticancer drugs in the conjugates. Complete killing of all target cells may not be essential since partial denudation of endothelium may result in an occlusive thrombus, and endothelial cells are unlikely to become resistant to anticancer agents nor to lose the targeting receptor. AAW93622-W93809 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying molecules that home to angiogenic vasculature used as targets
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour homing peptide; tumour; diagnosis; endothelial cell; breast; angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic; anti-arthritic; NGR receptor; inhibitor; angiogenesis; anticancer drug; prognosis; inflammation; regeneration; wounded tissue; targetting; macular degeneration; diabetic retinopathy; rheumatoid arthritis;
peptide can be linked to a moiety (e.g. doxorubicin), and used to direct
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel peptides which home to angiogenic
                                                                                                                             ö
                                                                                         Length 13;
                                                                                                                             2; Indels
                                                                                       5;
                                                                                       DB :
                                                                                                            Pred. No. 31;
1; Mismatches
                                                                                         Score 40;
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                                                                                                                                                                                                                                                                                          AAW93627 standard; protein; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Breast tumour homing peptide 1.
                                                                                         70.2%;
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                                                                                                                                                                                                                                                                                                                                                                 28-JUN-1999 (first entry)
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasqualini
                  the moiety to a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for anticancer agents.
                                                                                                                                                                                                CPRLCQSSC 13
                                                                                                                                                                1 CPRECESIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-215158/18.
                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  occlusive thrombus
                                                      Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                               AAW93627;
                                                                                         Query Match
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                                                                                                                             Matches
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(XI)a-FT-(X2)b, where: F1 = n Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1, -(L2)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L2)d-F2, 
                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; cytotoxic; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the
AAW93843-44 are examples of tumour homing peptides used in the invention
                                                                                                                                                             Gaps
                                                                                                                                                             ö
                                                                                                                                                             2; Indels
                                                                                                         Length 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Integrin-binding peptide sequence SEQ ID NO:1071.
                                                                                                         5
                                                                                                       DB:
                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone TC;
                                                                                                       Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 39; Page 589; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AAB17959 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US025044.
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                                                                                                       70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                    CPRLCQSSC 13
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                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                 1 CPRECESIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C,
                                                         Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17959;
                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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Gaps

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The present invention describes composition of matter (I) comprising an C domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = n Fc domain, X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1

C d, e, and f = are each independently 0 or 1, provided that at least 1

C c, d, e, and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA46431 to AAA69526 and AAB16955 to AAB18003 represent uncleotide and anino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythxopoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                        Gaps
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  Score 40; DB 3; Length 13;
Pred. No. 31;
                                        2; Indels
                                                                                                                                                                                                                                                                                                                                VEGF antagonist peptide sequence SEQ ID NO:1027.
                                        Mismatches
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                                                                                                                                                                                                              AAB17923 standard; peptide; 13 AA.
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99US-00428082.
70.2%;
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                                        Conservative
                                                                                                                CPRLCQSSC 13
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Query Match
Best Local Similarity
Matches 6; Conserv
                                                                            1 CPRECESIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
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Score 40; DB 3; Length 13; Pred. No. 31;

70.2%;

Query Match Best Local Similarity

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2; Indels
1; Mismatches
                                                                                            Search completed: November 16, 2004, 14:24:26 Job time : 59.283 secs
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Matches
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Sequence 2, Appli
Sequence 2, Appli
Sequence 1071, Ap
Sequence 57784, A
Sequence 3784, A
Sequence 37, Appl
Sequence 27, Appl
Sequence 196, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                            2004, 14:16:01; Search time 12.7358 Seconds (without alignments)
46.865 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-926-914-2
US-09-428-0828-1071
US-09-270-767-57784
US-09-252-991A-26031
US-09-252-991A-26031
US-09-055-699-37
US-09-055-538-37
US-09-661-468-37
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US-08-926-914-27
US-09-107-532A-3965
US-08-480-640A-196
US-08-68-968C-196
US-08-488-237A-196
US-08-472-9921-196
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US-09-538-092-995
US-09-543-681A-5457
US-09-139-802-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-153-927-2
US-09-565-918-5
                                                                                                                                                                                                        478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
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seq length: 200000000
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57
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Match Length DB
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                                                                             November 16,
                                                                                                                                                                        BLOSUM62
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Perfect score:
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No.
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GENERAL INFORMATION:
APPLICANT: Racaptalini, Erkki
APPLICANT: Ragadalini, Renate
FILE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
FILE REPERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Sequence 5, Appli
Sequence 2, Appli
Sequence 5, Appli
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Sequence 5, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 16, Appli
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| Sequence 2, Application US/09659786
| Sequence 2, Application US/09659786
| Sequence 2, Application US/09659786
| GENERAL INFORMATION:
| APPLICANT: Ruoslahti, Erki
| APPLICANT: Rasqualini, Renata
| TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
| TITLE OF INVENTION: Molecules That Home to Anglogenic Vasculature Using
| FILLE REPERENCE: P.LJ 3200
| FILLE REPERENCE: P.LJ 3200
| CURRENT APPLICATION NUMBER: US/09/659,786
| CURRENT PILING DATE: 2000-09-11
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Sequence 10,
                                         Sequence Seq
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Sequence 2
Sequence 5
Sequence 5
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US-09-139-802-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                             US-09-557-908-4
US-09-874-138-5
US-09-333-966-4
US-08-815-469-2
US-09-333-966-2
US-09-333-966-2
US-09-131-150-2
US-09-134-000C-5543
US-09-134-000C-5543
US-09-134-868-5
US-09-538-092-206
US-08-538-092-206
US-08-538-092-206
US-08-118-432-16
US-08-118-432-16
US-08-08-39-804-19
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Patent No. 6180084
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CPRLCQSSC 13
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Matches 6; Conserv
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US-09-428-082B-1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rucelahti, Erkki
APPLICANT: Rucelahti, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-09-659-786-2
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                                                                                                                                                                                                                                                                                                                  Score 40; DB 4; Length 13;
Pred. No. 8.2;
1; Mismatches 2; Indels
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ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997

"ASSTRICATION: 435
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PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LT
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08926914 Patent No. 6576239
                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 13 amino acids
TYPE: amino acid
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MOLECULE TYPE: peptide
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CPRLCQSSC 13
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5 CPRLCQSSC 13
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Matches 6; Conserv
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57784
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-05-270-767-42488

Sequence 42488, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REPRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
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       sequence 10.1, Application US/U9428U8ZB
Fatent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: CHEETHAN, JANET C.
APPLICANT: CHEETHAN, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: NUMBER: US/09/428,082B
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT PILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PLEMETIN Version 3.1
SEQ ID NO 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 4; Length 58; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 4; Length 13;
Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-09-428-082B-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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Patent No. 6703491
; Sequence 1071, Application US/09428082B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57784
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
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39 CPREFEPVC 47
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                                                                                                                                                                                                                                                                                             Length 816;
                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                             70.2%; Score 40; DB 2; I 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Teutomu, FUJIWARA
APPLICANT: Takeshi, WATANABE
APPLICANT: Masato, HORIE
APPLICANT: Toyomasa, KATAGIRI
ITILE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/09055699 Patent No. 6005088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELER: (491103
TELER: 6491103
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                         TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                         : 816 amino acids
amino acid
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TYPE: amino acid
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6, Conservative
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; MOLECULE TYPE: protein
US-08-820-170A-37
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MOLECULE TYPE: protein
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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US-09-055-699-37
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| Sequence 26031, Application US/09252991A
| Sequence 26031, Application US/0925291A
| Sequence 26031, Application US/0925291A
| GENERAL INFORMATION: Without and Amino ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| LENGTH 596
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                                                                                                                                                         70.2%; Score 40; DB 4; Length 118; 66.7%; Pred. No. 53; 2; Indels ative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TSULONU, FUJIWARA
APPLICANT: TSULONU, WATANABE
APPLICANT: TAKESHI, WATANABE
APPLICANT: TAKESHI, WATANABE
APPLICANT: TOYOMASS, HORIE
APPLICANT: TOYOMASS, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCES: 42
CORRESPONDENCES: 42
CORRESPONDENCES: ADDRESSE: SUGNETO, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTX: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CORPUTER: IBM PC COMPATIBLE
CORPUTER: IBM PC COMPATIBLE
CORPUTER: TEMP PC-TOCANAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/820,170A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 4; I
Pred. No. 2.1e+02;
1; Mismatches 1;
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                                                                                   ; ORGANISM: Drosophila melanogaster
US-09-270-767-42488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42488
LENGTH: 118
                                                                                                                                    Query Match
Best Local Similarity 66.7-
                                                                                                                                                                                                                                                                             |||| | :|
39 CPREFEPVC 47
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2; Mismatches
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                                                                                                                                                                     Sequence 37, Application US/09661468 Patent No. 6376189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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                               326 CCKECKSIC 334
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPRECESIC 9
1 CPRECESIC 9
                                                                                                                                                   US-09-661-468-37
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Patent No. 633404

GENERAL INFORMATION:
APPLICANT: WITHOUS TAKESHI
APPLICANT: WATANAEF, TSUTOMU
APPLICANT: HORAL, MASATO
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
CURRENT APPLICATION NUMBER: US/09/565,538
CURRENT FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-04-07
PRIOR PRILING DATE: 1999-04-07
PRIOR PRILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR PRILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR APPLICATION NUMBER: UF 69163/1997
                                                                                     GENERAL INFORMATION:
APPLICANT: FUJIWARA,
APPLICANT: FUJIWARA,
TEUTOMU
APPLICANT: FUJIWARA,
TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
ARAPLICANT: WASATO
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: 0-53599
CURRENT PAPLICATION NUMBER: 09/055,699
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER PELING DATE: 1998-04-07
EARLIER PELING DATE: 1997-03-19
EARLIER PELING DATE: 1996-03-19
EARLIER PELING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 816;
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                                           Sequence 37, Application US/09273565A Patent No. 6166190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 816
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Best Local Similarity 66.70
Thes 6; Conservative
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; ORGANISM: Homo sapiens
US-09-273-565-37
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US-09-565-538-37
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GENERAL INFORMATION:

APPLICANT: WATANABE, TSUTOWU

APPLICANT: WATANABE, TAKESHI

APPLICANT: WATANABE, TAKESHI

APPLICANT: WATANABE, TSUTOWU

APPLICANT: HORIE, MASATO

TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN

TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME

FILE REPRENCE: 0-5359

CURRENT PAPLICATION NUMBER: US/09/661,468

CURRENT PILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1997-03-19

PRIOR FILING DATE: 1996-03-19

PRIOR FILING DATE: 1996-03-19

PRIOR FILING DATE: 1996-03-19

PRIOR FILING DATE: 1997-03-05

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PARCHING UP OF IN OFF. 2.1

SEQ ID NO 37

LENGTH: 816
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APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WASATO
APPLICANT: WASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: Q-53599
CURRENT APPLICATION NUMBER: 09/565,538
FRIOR FILING DATE: 1090-04-05
PRIOR FILING DATE: 1090-04-07
PRIOR FILING DATE: 1990-04-07
PRIOR FILING DATE: 1990-03-19
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN VAY. 2.1
SEQ ID NO 37
LENGTH BASE
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US-09-976-165-37

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Search completed: November 16, 2004, 14:32:11 Job time : 14.0692 secs
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5457
LENGTH: 723
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                                                                                                                                                                               US-09-538-092-995

Sequence 995, Application US/09538092

Sequence 995, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Glot, Loic

APPLICANT: Glot, Loic

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TITLE REFRENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR PELING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 995

LENGTH: 699

TUDE OF SEQ ID NOS: 1387

TUDE OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9
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Score 40; DB 4; Length 816;
Pred. No. 2.7e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.4%; Score 39; DB 4; Length 699
Best Local Similarity 55.6%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

; LOCATION: (0)...(0)

; OTHER INFORMATION: Polypeptide Accession Number P23327

US-09-538-092-995
  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

ORGANISM: Proteus mirabilis
US-09-543-681A-5457
                                                                                                                     326 CCKECKSIC 334
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665 CPLVCETVC 673
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141 CPRNLEAIC 149
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ORGANISM: Homo sapiens
FEATURE:
                                                                                            1 CPRECESIC 9
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2, Appli 2, Appli 220960,

Sequence Sequence

Sequence 2, Appliance 220960, Sequence 122, Appliance 122, Appliance 124, Appliance 124, Appliance 124, Appliance 125, Appliance 125, Appliance 125, Appliance 125, Appliance 1364, Appliance

5 US-10-645-761-1071
5 US-10-666-696-1071
5 US-10-666-696-1071
5 US-10-666-696-1071
6 US-10-665-304-1071
6 US-10-375-992-2
6 US-10-375-992-2
6 US-10-3425-115-220960
0 US-09-488-783-122
0 US-09-892-877-121
7 US-10-112-944-828
1 US-10-112-944-828
1 US-10-112-944-828
1 US-09-764-868-764
1 US-09-764-868-764
1 US-09-764-868-764
1 US-09-815-242-1256-6642
1 US-09-815-242-1256-6642
1 US-09-916-136-4
1 US-09-916-136-4
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1 US-09-916-136-4
1 US-09-916-136-8

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US-10-363-204-123
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                                                                                                                                                                                                                                                                                                                                                                Sequence 123, App Sequence 127, App Sequence 125, App Sequence 516, App Sequence 521, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1071, Ap Sequence 1071, Ap Sequence 1071, Ap
                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                              (without alignments)
75.615 Million cell updates/sec
                                         ; Search time 42.1132 Seconds
                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                6 US-10-363-204-123
6 US-10-363-204-127
6 US-10-363-204-127
4 US-10-106-698-5476
4 US-10-043-487-521
5 US-10-424-599-206937
US-09-840-277-32
US-09-840-277-32
4 US-10-264-374-2
4 US-10-264-374-2
5 US-10-632-388-1071
5 US-10-651-723-1071
                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                         1568699 seqs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                         November 16, 2004, 14:30:02
                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                           Published Applications AA:*
                             - protein search, using sw model
                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                  seq length: 0
seq length: 200000000
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57
                                                                            1 CPRECESIC 9
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Match Length
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                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                     Score
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                                                                                                                                  Minimum DB
Maximum DB
                                                                             Sequence:
                                                                                                          Searched:
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ALIGNMENTS

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Sequence 123, Application US/10363204
Sequence 123, Application US/10363204
Publication No. US20040170955A1
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Human and Mouse Targeting Peptides Identified by Phage Display
FILE OF INVENTION: HUman and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 123
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100.0%; Score 57; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Peptide
J. COCATION: (1)..(9)
COTHER INFORMATION: synthetic construct
US-10-363-204-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 127, Application US/10363204
Publication No. US20040170955A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: HYBRIGENICS
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein interactions between Shigella Flexneri polypeptide
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin version 3.1
SEQ ID NO 521
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Scoulic David K
APPLICANT: Scoulic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/428
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206937
LENGTH: 10.2
TYPE: PRT
ORGANISM: Glycine max
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Pred. No. 25;
1; Mismatches 2; Indels
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_28891C.1.pep
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Publication No. US20030055220A1
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ORGANISM: Shigella Flexneri
           NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 5476
LENGTH: 58
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-106-698-5476
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NAME/KEY: unsure
LOCATION: (1)..(1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10. 1. Application US/10363204

Publication No. US20040170955A1

GENERAL INFORMATION:
APPLICAMY: Board of Regents, The University of Texas System
APPLICAMY: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774 P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2013-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 125
LENGTH: 31
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILLE REPERENCE: 005774-1003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFFWARE: PatentIn version 3.1
SEQ ID NO 127
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88.9%; Pred. No. 5.6;
artive 0; Mismatches
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; OTHER INFORMATION: synthetic construct
US-10-363-204-125
                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
US-10-363-204-127
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                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
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ASSULTA-2
Sequence 2, Application US/10264374
Sequence 2, Application US/10264374
Sequence 2, Application NO. US20030113320A1
Sequence 2, Application NO. US20030113320A1
Sequence 2, Application NO. US20030113320A1
SERBEAL INFORMATION:
APPLICANT: Rangualahi, Renata
TITLE OF INVENTION: NOR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/10/264,374
CURRENT FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: US/09/139,802
PRIOR PELING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1996-09-10
PRIOR FILING DATE: 1996-09-10
SPRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rucelahti, Erkki
APPLICANT: Rucelahti, Renata
Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
Derived Therefrom, and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-264-374-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 14; Length 13;
Pred. No. 28;
1; Mismatches 2; Indels
                    Score 40; DB 9; Length 13;
Pred. No. 28;
1; Mismatches 2; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 9122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/375,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/10375992; Publication No. US20030152578A1; GENERAL INFORMATION:
                    70.2%;
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ORGANISM: Artificial Sequence
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                         Query Match 70.2
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-10-375-992-2
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                                                 Query Match 71.9%; Score 41; DB 15; Length 102; Best Local Similarity 55.6%; Pred. No. 1.1e+02; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09765086

Batent No. US2001046498Al
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosqualini, Renata
APPLICANT: Wadih, Arap
APPLICANT: Bacdesn, Dale E.
APPLICANT: Bllerby, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apoptotic Activity
FILE REPERENCE: P-LJ 3844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 70.2%; Score 40; DB 9; Length 13; Best Local Similarity 66.7%; Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: FEIGE, ULRICH
APPLICANT: MACEY, DAVID LEE
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
FILE REFREENCE: A-689A
CURRENT APPLICATION NUMBER: US/09/840,277
CURRENT FILING DATE: 2001-08-14
FRIOR APPLICATION NUMBER: 60/198,919
FRIOR APPLICATION NUMBER: 60/198,919
FRIOR APPLICATION NUMBER: 60/201,394
FRIOR APPLICATION NUMBER: 60/201,394
FRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 32
SEQ ID NO 32
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; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT FILING BATE: 2001-011-17
PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: synthetic peptide US-09-765-086-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09840277
Patent No. US20020168363A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-424-599-206937
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                                                                                                                                                                                                                                                                              RESULT 7
US-09-765-086-2
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Gaps

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; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-10-632-388-1071
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-10-651-723-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1071, Application US/10651723
Publication No. US20040057953A1
                                                                                                                                                                                                                                                                                                                                                                                                           70.2%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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Publication No. US20040044188A1

GENERAL INFORMATION:

APPLICANT: ESIGE, ULEICH

APPLICANT: LIU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

APPLICANT: BOONE, THOMAS C.

APPLICANT: BOONE, THOMAS C.

APPLICANT: GOONE, THOMAS C.

CURRENT APPLICANTION: WODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527

CURRENT FILING DATE: 2003-06-27

PRIOR APPLICATION NUMBER: US/10/609, 217

CURRENT FILING DATE: 1999-10-22

PRIOR FILING DATE: 1999-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.2%; Score 40; DB 15; Length 13; 66.7%; Pred. No. 28; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              70.2%; Score 40; DB 14; Length 13; 66.7%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                        APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (619) 535-9901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                          TOPOLOGY: both
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1071, Application US/10632388
; Publication No. US20040053845A1
FILING DATE: 27-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acid
TYPE: amino acid
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1071
LENGTH: 13
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5 CPRLCQSSC 13
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA

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APPLICANT: CHEETHAM, JANET C.

APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REPERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/632,388
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR APPLICATION NUMBER: (6/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PALENTIN VERSION 3.1
LENGTH: 13
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Pred. No. 28;
1; Mismatches 2; Indels
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APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
ITTLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
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; Publication No. US20040077022A1
; GENERAL INFORMATION:
    APPLICANT: FEIGE, ULRICH
; APPLICANT: CHESTHAM, JANET C.
APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; PRICANT: GUDAS, JEAN WARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; PRICANT: GUDAS, JEAN WABER:
; TITLE OF INVENTION: WUMBER: US/10/666,696
; CURRENT APPLICATION NUMBER: US/209563,286C
; PRIOR PILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-23
; NUMBER OF SEQ ID NOS: 1157
; SEQ ID NO 1071
; LENGTHAN: 13
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APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REPERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/645,761
CURRENT FILING DATE: 2003-08-18
FRIOR PELLOR POWBER: US/09/428,082B
FRIOR PILING DATE: 1999-10-22
FRIOR PILING DATE: 1998-10-23
FRIOR FILING DATE: 1998-10-23
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70.2%; Score 40; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels
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Job time : 44.1132 Becs
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ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7
Matches 6; Conservative
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5 CPRLCQSSC 13
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5 CPRLCQSSC 13
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1: /cgn2_6/ptodata/1/paa/BCG_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USGG_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

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8: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

9: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

17: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

18: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

19: /cgn2_6/ptodata/1/paa/USGB_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/USGBB_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/USGBB_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/USGBB_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

17: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

18: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

19: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

17: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

18: /cgn2_6/ptodata/1/paa/USGBC_COMB.pep:*

18: /cgn2_6/ptodata/1/
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6730630 segs, 1107998698 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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57
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                 OM protein
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                                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	QI	Description
-	57	100.0	6	П.	-27692A-	Sequence 123, App
C1 F	57	100.0	on 0	100	PCT-US02-27836-56	Sequence 56, Appl Sequence 123, App
J 44	57	100.0	<i>y</i> 0	33,7	US-10-784-537-2	Sequence 2, Appli
ß	20	87.7	13	-	PCT-US01-27692A-127	Seguence 127, App
91	200	87.7	13	- 6	PCT-US02-27836-60	Sequence 60, Appl
- α	ח ני	97.7	1 [	7 6	US-10-363-204-12/ IIS-10-784-537-3	Semience 127, App
9 00	7.4	82.5	3.5	G -	PCT-US01-27692A-125	Sequence 125, App
10	47	82.5	31	н	PCT-US02-27836-58	Sequence 58, Appl
# :	7 4 7	82.5	31	2,0	US-10-363-204-125	Sequence 125, App
13	47	82.0	3 7	9 6	US-10-784-537-1 US-10-784-537-9	Sequence 1, Appli Sequence 9, Appli
14	4	77.2	7	33	US-10-784-537-5	Sequence 5, Appli
15	4.	77.2	ထင္	33	US-10-784-537-6	Sequence 6, Appli
17	4 4 4 4	2.77	, r,	27	FCT-0S00-26524B-5466 US-10-106-698-5476	Sequence 5455, Ap Sequence 5476. Ap
18	43	75.4	68	26	US-10-043-487-521	Sequence 521, App
19	43	75.4	460	18	US-09-488-725A-1885	Sequence 1885, Ap
20	<b>4.</b> 4	75.4	460	2 28	US-10-258-898A-1885 HS-10-286-897-1885	Sequence 1885, Ap Sequence 1885, Ap
7 7 7	4.4	75.4	512	1 8	US-09-488-725A-5457	Sequence 5457, Ap
23	43	75.4	512	78	US-10-258-898A-5457	Sequence 5457, Ap
24	43	75.4	512	28	US-10-286-897-5457	Sequence 5457, Ap
52.5	4 4	71.9	8 8	7 6	US-U9-758-439-1223 US-10-201-915-1223	Sequence 1223, Ap
27	41	71.9	98	28	US-10-221-279-12244	Sequence 12244, A
28	41	71.9	102	30	US-10-424-599-206937	Sequence 206937,
3.0	4.4	71.9	171	٦,	PCT-US99-22853B-1877 PCT-US99-22853B-1876	Sequence 1877, Ap
31	41	71.9	181	77	US-09-724-676-88311	Sequence 88311, A
32	41	71.9	181	21	US-09-724-676-88324	Sequence 88324, A
33	41	71.9	181	22	US-09-724-676A-88311	Sequence 88311, A
4. C	4	7.7.	181	2 7	US-US-124-6/6A-88324 TR-10-120-205E-30329	Sequence 30329. A
9 6	7 T	71.0	1 6	ù -	DCT-11599-228538-1875	Semience 1875. An
37	4 4	71.9	399	36	US-60-550-051-290	Sequence 290, App
38	41	71.9	649	36	US-60-581-351-5898	Sequence 5898, Ap
39	40	70.2	ដ	н,	PCT-US00-01602-2	Sequence 2, Appli
<b>4</b> 4	04.4	7.07	7 5	٦.	PCT-US99-25044-102/ DCT-TG99-25044-1071	eda
4 4	4.0	70.2	3 2	. =	US-08-710-067-5	Sed
43	40	70.2	13	v	US-09-235-902-2	Sequence 2, Appli
4 4 4 0	4 4 0 0	70.2	13	18	US-09-489-582-2 US-09-563-286B-1071	Sequence 2, Appli Sequence 1071, Ap
1	?		) i	١.		
					ALIGNMENTS	
RESULT 1	ULT 1	103				
; Sequence	ze 123,	Applic	ation P	C/TL	IS0127692A	
	LINFORM	ATION		. '		
, APPLICANT	CANT: BC	: Board of	Regent	8, J	ö	: Texas System Dentides Identified by Phage Display
FILE	SEFERENC	E: 005	774 . P00	3PC	Į.	Indian of the continuous
, CURRE	NT APPLI	CATION	NUMBER	٠. د	CURRENT APPLICATION NUMBER: PCT/USO1/27692A	
NUMBE	OF SEC	ON CI	S: 251		<b>&gt;</b>	
,	ARE: Pat	entIn	version	3.1		
U)	NO 123					
TYPE	. PRT					
; ORGANISM: Artificial S	NISM: Az	tifici	al Sequenc	ence		
NAME,	/KEY: Pe	ptide				
LOCAL	LION: (1	(6)	•			
; PCT-TS01-	1 INFORM	ATION:	synthetic	CIC	construct	
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TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display FILE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display FILE REFERENCE: 005774.P003PCT CURRENT APPLICATION NUMBER: PCT/US01/27692A CURRENT FILING DATE: 2001-09-07 NUMBER OF SEQ ID NOS: 251
SOFTWARE: PatentIn version 3.1
SEQ ID NO 127
LENGTH: 13
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                                                                                                                                                                                                         Sequence 2, Application US/10784537

Sequence 2, Application US/10784537

GENERAL INFORMATION:

APPLICANT: ARAP, WADIH

APPLICANT: PASQUALINI

APPLICANT: LAHDENRANTA, JOHANNA

TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARCETING PEPTIDES

TITLE OF INVENTION: AMINOPEPTIDASE A (APA)

TITLE OF INVENTION: AMINOPEPTIDASE A (APA)

TITLE OF INVENTION: AMINOPEPTIDASE A (APA)

TITLE OF INVENTION: AMINOPEPTIDASE

CURRENT PLILNG DATE: 2004-02-23

CURRENT FILING DATE: 2002-08-30

PRIOR PLILNG DATE: 2002-08-08

PRIOR PLILNG DATE: 2000-09-08

PRIOR PLILNG DATE: 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(13); COTHER INFORMATION: Synthetic construct PCT-US01-27692A-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 8; Conserva
                                                        1 CPRECESIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kolonin, Mikhail G. (applicant for the United States of America (applicant for the purpose of the United States of America only)

TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla TITLE OF INVENTION: and Adipose Tissues
FILE REPERENCE: 5774,0009PCT
CURRENT APPLICATION NUMBER: PCT/USO2/27836
FRIOR FILING DATE: 2002-08-30
PRIOR PLING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 144
SEQ ID NO 56
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: Bornoses of all designated states except US)
APPLICANT: Parqualini, Renata (applicant for the purpose of the United States of APPLICANT: Arap, Wadih (applicant for the purpose of the United States of AMPLICANT: Only)
APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of AMPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of AMPLICANT: America only)
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                               Length 9;
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                        Query Match
100.0%; Score 57; DB 1; I
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 9; Conservative 0; Mismatches 0;
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NAME/KEY: Peptide

LOCATION: (1)..(9)

OTHER INFORMATION: synthetic construct
US-10-363-204-123
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Application PC/TUS0227836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic Peptide
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; Sequence 123, Application US/10363204
; GENERAL INFORMATION:
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SEQ ID NO 123
LENGTH: 9
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Best Local Similarity الاست
الاستارية 9; Conservative
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APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774,P003PCT
CURRENT APPLICATION NUMBER: PCT/US01/27692A
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: PatentIn version 3.1
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                                US-LU-/84-53/-3

Sequence 3. Application US/10784537

GENERAL INFORMATION:
APPLICANT: ARAP, WADIH
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: LAHDENRANTA, JOHANNA
TITLE OF INVENTION: ANINOPERTIDASE A (APA) TARGETING PEPTIDES
CURRENT PELLICATION NUMBER: US/10/784,537
CURRENT PILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
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COTATION: (1)...(31)
COTHER INFORMATION: synthetic construct
PCT-US01-27692A-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserva
                    US-10-784-537-3
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TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla TITLE OF INVENTION: and Adipose Tissues
FILE REFERENCE: 5774.P009PCT
CURRENT APPLICATION NUMBER: PCT/US02/27836
CURRENT FILING DATE: 2002-08-30
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GEQUENCE 127, Application US/10363204
GEQUENCE INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFREENCE: 2003-03-07
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SSOFTWARE: PatentIn version 3.1
SEQ ID NO 127
LENGTH: 13
                                                                                                                                                                                                                                                    APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: purposes of all designated states except US)
APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
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88.9%; Pred. No. 2.2;
tive 0; Mismatches
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88.9%; Pred. No. 2.2;
tive 0; Mismatches
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PRIOR FILING DATE: 2001-09-07
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COCATION: (1)..(13);
CTHER INFORMATION: Synthetic construct
US-10-363-204-127
                                                                                                                                                                   PCT-US02-27836-60; Sequence 60, Application PC/TUS0227836; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 144
SOFWHARB: Patentin version 3.1
SEQ ID NO 60
LENGTH: 13
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
                             5 CPRECESNC 13
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APPLICANT:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide
US-10-784-537-1
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GENERAL INFORMATION:

APPLICANT: ARAP, WANIH

APPLICANT: ARAPLANIH

APPLICANT: MARCHIO, SERENA

APPLICANT: MARCHIO, SERENA

APPLICANT: MARCHIO, SERENA

TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES

TITLE OF INVENTION: AMINOPEPTIDASE

CURRENT APPLICATION NUMBER: US/10/784,537

CURRENT FILING DATE: 2004-02-23

PRIOR APPLICATION NUMBER: PCT/US01/27692

PRIOR APPLICATION NUMBER: 60/231,266

PRIOR PELING DATE: 2000-09-08

PRIOR PELING DATE: 2000-09-08

PRIOR PELING DATE: 2000-09-08

PRIOR PELING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,266

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APPLICANT: PASQUALLINI
APPLICANT: PASQUALLINI
APPLICANT: AARDENRANTA, JOHANNA
TITLE OF INVENTION: AMINOBEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: POR THE TREATMENT OF CANCER
TITLE OF INVENTION: POR THE TREATMENT OF CANCER
FILE REFERENCE: UTSC: 491.05.3
CURRENT APPLICATION NUMBER: US/10/784,537
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-08
PRIOR FILING DATE: 2001-09-08
PRIOR FILING DATE: 2001-01-17
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ORGANISM: Artificial Sequence
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APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of APPLICANT: America only)
TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against PlaTITE OF INVENTION: and Adipose Tissues
FILE REFERENCE: 5774.P009PCT
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GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INTERTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774, P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 125
                                                                                                                                                                                                                                                               America only)
Arap, Wadih (applicant for the purpose of the United States of America
                                                                                                                                     APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: purposes of all designated states except US)
APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of
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CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: PCT/US01/27692
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
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i OTHER INFORMATION: synthetic construct
US-10-363-204-125
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                                                                Application PC/TUS0227836
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Sequence 1, Application US/10784537
; SENERAL INFORMATION:
; APPLICANT: ARAP, WADIH
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PASCUALINI
APPLICANT: PASCUALINI
APPLICANT: MACHIO, SERENA
APPLICANT: LAHDENRANTA, JOHANNA
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION NUMBER: BCT/USO1/27692
PRIOR PELLING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
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APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: ARCHIO, SERBNA
TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: POR THE TRRATMENT OF CANCER
TILLE OF INVENTION: POR THE TRRATMENT OF CANCER
FILE REFRENCE: UTSC: 912US
CURRENT APPLICATION NUMBER: US/10/784,537
CURRENT APPLICATION NUMBER: PCT/US02/27836
PRIOR FILING DATE: 2004-02-33
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR FILING DATE: 2001-09-09
PRIOR FILING DATE: 2001-09-09
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
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                             1; Indels
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                      US-10-784-537-5; Sequence 5, Application US/10784537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10784537
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 7
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                    CPRECESIC 9
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prior Filing Date: 2000-09-08

prior Filing Date: 2000-09-08

programmer of SEQ ID NOS: 13

programmer of SEQ ID NOS: 13

programmer of SEQ ID NO 6

programmer of SEQ ID NO 6

programmer of Artificial Sequence

programmer of Sequence

programmer
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OTHER INFORMATION: Synthetic Peptide US-10-489-071-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CPRECESIC 9
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US-10-489-071-60
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Sequence 60, Appl
Sequence 18045, A
Sequence 26, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 22, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 22211, A
Sequence 22211, A
Sequence 24597, A
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 282, Appl
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                                                                                                                                     November 16, 2004, 14:24:42; Search time 4.07547 Seconds (without alignments) 40.083 Million cell updates/sec
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1: /cgn2 6/ptodata/1/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/1/paa/US06_NEW COMB.pep:*

3: /cgn2 6/ptodata/1/paa/US07_NEW COMB.pep:*

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7: /cgn2 6/ptodata/1/paa/US10_NEW COMB.pep:*

8: /cgn2 6/ptodata/1/paa/US11_NEW COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-489-071-56
US-10-489-071-60
US-10-489-071-60
US-10-220-366A-18045
US-10-220-366A-26731
US-09-993-2348-6
US-10-411-9108-48
US-10-765-727-23
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US-10-976-102-89
US-10-976-103-89
US-10-970-847-38
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US-10-95-952-282
US-10-96-241-38
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 CPRECESIC 9
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Perfect score:
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                                                                                                                                          Run on:
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26 34 59.6 365 6 US-10-732-923-16980 Sequence 16980, A 28 34 59.6 818 6 US-10-732-923-14186 Sequence 14186, A 29 34 59.6 818 6 US-10-732-923-14187 Sequence 14187, A 29 34 59.6 813 6 US-10-732-923-14221 Sequence 14221, A 30 34 59.6 1104 6 US-10-732-923-14222 Sequence 14221, A 34 59.6 1104 6 US-10-732-923-14222 Sequence 14222, A 34 59.6 1114 6 US-10-732-923-14219 Sequence 14219, A 34 59.6 1119 6 US-10-732-923-14219 Sequence 14219, A 34 59.6 1120 6 US-10-732-923-14219 Sequence 14219, A 35 57.9 13 1 PCT-10540-34918-19 Sequence 19, Appl 37 37 57.9 13 6 US-10-976-140-19 Sequence 19, Appl 40 33 57.9 80 6 US-10-976-160-160 Sequence 15, Appl 40 33 57.9 81 6 US-10-732-923-156-15 Sequence 15, Appl 41 33 57.9 184 6 US-10-732-923-3520 Sequence 15, Appl 41 33 57.9 184 6 US-10-732-923-3520 Sequence 15, Appl 41 33 57.9 184 6 US-10-732-923-3520 Sequence 165, Appl 44 33 57.9 184 6 US-10-732-923-3520 Sequence 105, Appl 44 33 57.9 184 6 US-10-732-923-3520 Sequence 105, Appl 44 33 57.9 461 6 US-10-735-256-4 Sequence 105, Appl 50 US-10-735-256-9 Sequence 105, Appl 50 US-10-735-256-9 Sequence 105, Appl 50 US-10-735-256-9 Sequence 105, Appl 50 US-10-735-256-4 Sequence 105, Appl 50 US-10-735-256-9 Sequence 105, Appl
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## ALIGNMENTS

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REBULT 1

Sequence 55, Application US/10489071

Sequence 55, Application US/10489071

SEQUENCE INVERVATION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST TITLE OF INVERVATION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST TITLE OF INVERTION: COMPOSITIONS AND METHODS OF TISSUES

CURRENT PELLOCATION NUMBER: US/10/489,071

CURRENT PELLOCATION NUMBER: US/10/489,071

PRIOR FILING DATE: 2002-08-30

WOMER OF SEQ ID NOS: 144

SOUTHARE: Pacentin Version 3.1

LENGTH: 9

SOUTHARE: Pacentin Version 3.1

PERJURE: PERJURE: PACENTING DATE: 2002-08-30

OGNER INFORMATION: Synthetic Peptide

US-10-489-071-56

OGNER LOCAL SIMILATITY 100.0%; Pred. No. 7.48+04;

MATCHES 9; CONSERVATION: WISMATCHES 0; Mismatches 0; Indels 0; Gaps 0;

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Pred. No. 51;
                                                                                                                                                                                                   APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFRENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT PILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: Custom
SEQ ID NO 26731
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORCANISM: Homo sapiens
PRATURE:
NAME/KEY: misc_feature
LOCATION: (1) ... (388)
CTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-26731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234B
FILLING DATE: 19-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/828683
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                Sequence 26731, Application US/10220366A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09993234B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.9%;
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Best Local Similarity 55.0
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                                                                53 CAROCVSVC 61
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                           CPRECESIC
                                                                                                                                                 US-10-220-366A-26731
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US-09-993-234B-6
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TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
CURRENT APPLICATION NUMBER: US/10/489,071
FRICA RAPLICATION NUMBER: PCT/USO2/27836
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PATENTIN VETSION 3.1
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; Sequence 18045, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; PILE REPERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR PILING DATE: 2000-05-18
; PRIOR PILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: CUSTOM
; SEQ ID NO 18045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 6; Length 143;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 6; Length 31; Pred. No. 0.15;
                                                                                                        Score 50; DB 6; Length 13;
Pred. No. 0.024;
0; Mismatches 1; Indels
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; OTHER INFORMATION: Xaa = any amino acid or nothing US-10-220-366A-18045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                         ) OTHER INFORMATION: Synthetic Peptide US-10-489-071-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Synthetic Peptide US-10-489-071-58
                                                                                                                                                                                                                                                                                                                              Sequence 58, Application US/10489071 GENERAL INFORMATION:
                                                                                                        87.78;
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55.6%;
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.5
Local 8, Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                  CPRECESNC 13
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LENGTH: 31
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i TYPE: PRT
   ORGANISM: Homo sapiens
US-10-765-727-23
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US-10-976-102-78
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APPLICANT: BRIEND, EMMANUGE CYRILLE PASCAL

APPLICANT: CHAMPION, RRIAN ROBERT

APPLICANT: CHAMPION, RIAN ROBERT

APPLICANT: CHAMPION, RIAN ROBERT

APPLICANT: CHAMPION, BRIAN ROBERT

TITLE OF INVENTION: WODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY

TITLE REFERENCE: 674525-2010

CURRENT PILING DATE: 2004-01-23

FRICA PAPLICATION NUMBER: PCT/GB02/03426

FRICA PAPLICATION NUMBER: GB 0118153.6

FRICA PAPLICATION NUMBER: GB 0118153.6

FRICA RELING DATE: 2002-04-05

FRICA RELING DATE: 2002-04-05

FRICA RELING DATE: 2002-05-28

FRICA RELING DATE: 2002-05-38

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US-10-411-910B-48

Sequence 48, Application US/10411910B

GENERAL INFORMATION;

APPLICANT: Dillon, Harrison F.

TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes

FILE REFERENCE: H2041203-P

CURRENT APPLICATION NUMBER US/10/411,910B

CURRENT APPLICATION NUMBER US/10/411,910B

NUMBER OF SEQ ID NOS: 363

SEQ TEMPLE PATENTIN VERSION 3.2

SEQ ID NO 48

LENGTH: 844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
   REFERENCE/DOCKET NUMBER: P1007P1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: Amino Acid
TOPOLLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ; ORGANISM: Desulfitobacterium hafniense US-10-411-910B-48
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; Sequence 23, Application US/10765727
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
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187 CPERCAAVC 195
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Score 37; DB 6; Length 2471;
Pred. No. 2.8e+02;
1; Mismatches 1; Indels
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; Sequence 78, Application US/10976102
; GENERAL INFORMATION:
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: USe
; TITLE OF INVENTION: USe
; TITLE OF INVENTION: USe
; TITLE OF INVENTION: UNMER: US/10/976,102
CURRENT PILING DATE: 2004-10-27
; PRIOR PELLING DATE: 2001-09-11
; PRIOR PILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
; LENTH: 106
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75.0%; Pred. No. 2.8e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   Sequence 57, Application US/10846989;
GENERAL INFORMATION:
APPLICANT: BOLDMER, MARK WILLIAM
APPLICANT: BRIEND, EMWANUEL CYRILLE PASCAL
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: TUGAL, TAWARA
APPLICANT: TUGAL, TAWARA
APPLICANT: TUGAL, TAWARA
APPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: WEDICAL TREATMENT
FILE OF INVENTION: 654525-2012
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: BOT/GB02/05133
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR PILING DATE: 2002-11-14
PRIOR PILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-010
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PATENTIN UNER: GB 0220913.8
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PATENTIN UNER: GB 0220913.8
TYPE: PRI
TYPE: PRI
TYPE: PRI
CREATH: 2471
TYPE: PRI
CREATH: 2471
       64.9%;
75.0%;
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ORGANISM: Arabidopsis thaliana
       Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conservative
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1371 PRDCESGC 1378
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APPLICANT: HYSEQ, INC

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REPRENCE: 21272-042

CURRENT APPLICATION NUMBER: US/10/220,366A

CURRENT FILING DATE: 2002-08-28

PRIOR APPLICATION NUMBER: 09/517,409

PRIOR FILING DATE: 2000-05-18

PRIOR PILING DATE: 2000-05-18

PRIOR PILING DATE: 2011-02-23

NUMBER OF SEQ ID NOS: 27802

SEQ ID NO 22211

LENGTH: 64
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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NAME/KEY: misc_feature

LOCATION: (1)...(64)

OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-22211
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                                                                                                                              ; Sequence 22211, Application US/10220366A; GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-10-976-102-89
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Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-10-220-366A-17365
                                                                 RESULT 13
US-10-220-366A-22211
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; Sequence 96, Application US/10976102
; GENERAL INFORMATION:
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: Use
; TITLE OF INVENTION: Use
; FILE REFERENCE: 1278D
; CURRENT APPLICATION NUMBER: 09/950,933
; PRIOR FILING DATE: 2004-10-27
; PRIOR PILING DATE: 2000-09-13
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 106
; TWOR: DATE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: Use
FILE REFERENCE: 1278D
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT FILING DATE: 2004-10-27
PRIOR APPLICATION NUMBER: 60/950,933
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/232,569
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
SROID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                             Query Match 63.2%; Score 36; DB 6; Length 80; Best Local Similarity 55.6%; Pred. No. 17; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 6; Length 80;
Pred. No. 17;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 79, Application US/10976102; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Arabidopsis thaliana US-10-976-102-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana US-10-976-102-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 CPSECDRRC 56
                                                                                                                                                                                                                                                                 48 CPSECDRRC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CPRECESIC 9
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                                                                                                                                                                                                   1 CPRECESIC 9
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-10-976-102-79
US-10-976-102-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Gaps

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APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antinicrobial Peptides and Methods of TITLE OF INVENTION: Use
FILE REFERENCE: 1278D
GURRENT APPLICATION NUMBER: US/10/976,102
CURRENT APPLICATION NUMBER: 09/950,933
PRIOR APPLICATION NUMBER: 09/950,933
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/232,569
PRIOR FILING DATE: 2000-09-13
SPRIOR FILING DATE: 2000-09-13
SPRIOR FILING DATE: 2000-09-13
SOFTWARE: PASSEGE FOR WINDOWS VERSION 4.0
SEQ ID NOS: 99
LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 6; Length 80; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 17365, Application US/10220366A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HYSEQ, INC
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48 CPSECDRRC 56

ď

Search completed: November 16, 2004, 14:47:12 Job time : 4.07547 secs

60 CAHDCDNIC 68

g

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

November 16, 2004, 14:15:03; Search time 10.1887 Seconds (without alignments) 84.991 Million cell updates/sec Run on:

US-10-784-537-2 57 1 CPRECESIC 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	47	82.5	425	10	AE2094	hypothetical prote
N	41	71.9	273	~	T16246	
e	40	70.2	395	~	S75952	hypothetical prote
4	40	70.2	487	7	T34868	probable glutamate
ς,	40	70.2	487	7	B89813	NADH-glutamate syn
9	40	70.2	488	~	F86916	NADH-dependent glu
7	40	70.2	835	~	JP0076	in - c
80	40	70.2	3133	~	S52093	hemocytin - silkwo
თ		68.4	211	-	WMBEMA	23.5K protein - Ma
10		68.4		-	WMBEMB	23.5K protein - Ma
11	39	68.4		7	T23802	hypothetical prote
12		68.4	669	~	A54660	histidine rich cal
13	39	68.4	852	~	A34373	histidine-rich cal
14	38	66.7	372	~	T23680	hypothetical prote
15	38	66.7	708	7	AE3407	formate dehydrogen
16	38	66.7	743	0	B97498	molybdopterin oxid
17	38	66.7	743	~	AG2716	reductase [importe
18	38	66.7	2219	~	T27684	hypothetical prote
19	37.5	65.8	290	~	G72858	AcOrf-70 protein -
20	37	64.9	209	0	F64416	polyferredoxin - M
21	37	64.9	457	~	T03449	protein V - Hendra
	37	64.9	474	~	E75069	glutamate synthase
23	37	64.9	475	~	B75024	
24	37	64.9	488	7	B75551	
25	37	64.9	489	7	F82085	
56	37	64.9	554	~	T25288	hypothetical prote
27	37	64.9	573	7	JC4335	anti-mullerian hor
28	37	64.9	859	~	869700	hypothetical prote
59	37	64.9	888	~	H88085	protein TilFi.8 (i

hypothetical protein F35A5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T16246
R;Leimbach, D.
submitted to the EMBL Data Library, January 1996
R;Leimbach, D.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z18485
A;Recession: T16246
A;Reference number: Z18485
A;Recession: T16246
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Caesidues: 1.273 <LEI>A;Residues: 1.273 <LEI>A;Cross-references: UNIPROT:Q20000; EMBL:U46675; NID:g1166613; PID:g1166614; PIDN:AAB526;
A;Experimental source: strain Bristol N2; clone F35A5
A;Genetics:
A;Genetics:
A;Genetics: X
A;Introns: 18/3; 62/3; 81/3; 100/3; 140/3; 226/2

71.9%; Score 41; DB 2; Length 273;

Query Match

hypothetical prote	transcription fact	GASA4 - Arabidopsi	gibberellin-regula	cytosolic acyl-CoA	probable acyl-coa	hypothetical prote	glutamate synthase	glutamate synthase	glutamate synthase	protein T23J18.22	hypothetical prote	hypothetical prote	hemagglutinin-neur	hemagglutinin-neur	EMP70 protein prec	
T19691	I38414	T49958	S60232	C81662	F71502	T32691	G98262	AC3022	AE3514	H86248	T46720	T15574	HNNZ39	A43487	S64915	
~	7	7	~	~	~	7	~	7	~	~	~	7	-	~	7	
1353	2109	106	106	159	160	413	484	484	499	522	539	567	575	575	667	
64.9	64.9	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	
37	37	36	36	36	36	36	36	36	36	36	36	36	36	36	36	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

Species: Species: Species: Note: No Note: No Notes:	
A; Decrees in Nostoc sp. strain PCC 7120 is a synonym C; Date: 14-Dec-2001 #sequence_revision 14-Dec-200 C; Accession: AE2094 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazaw DiA, Res. 8, 205-213, 2001 A; Title: Complete Genomic Sequence of the Filame A; Reference number: AB1807; MUD:21595285; PMID: A; Reference number: AB1807; MUD:21595285; PMID: A; Residues: 1-425 «KUR> A; Genetics: A; Conservative 0; Mismatches Qy I CPRECESIC 9	sp. (strain PCC 7120)
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-20 C,Accession: AE2094 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazaw DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filame A;Reference number: AB1807; MUD:21595285; PMID: A;Accession: AE2094 A;Stetus: preliminary A;Molecule type: DNA A;Residues: 1-425 «KUR» A;Residues: 1-425 «KUR» A;Cess-references: UNIPROT:Q8YUN1; GB:BA000019; A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr2308 Query Match Best Local Similarity 77.8%; Score 47; DB Best Local Similarity 77.8%; Pred. No. 5-4; Matches 7; Conservative 0; Mismatches	f Anabaena sp. strain PCC 7120
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, Nakazak, N.; Shimpo, S.; Sugimoto, M.; Takazak, DNA, Res. 8, 205-213, 2001. A;Title: Complete Genomic Sequence of the Filame A;Reference number: AB1807; MUD:21595285; PMID: A;Accessor. AE2094 A;Stetus: preliminary A;Molecule type: DNA A;Residues: 1-425 <kur> A;KOSS-references: UNIPROT:QBYUNI; GB:BA000019; A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr2308 Query Match Best Local Similarity 77.8%; Pred: No. 5.4; Matches 7; Conservative 0; Mismatches</kur>	1 #text_change 09-Jul-2004
DNA RESE. 8, 205-213, 2001 A,Title: Complete Genomic Sequence of the Filame A,Reference number: AB1807; MUID:21595285; PMID: A,Actatus: preliminary A,Rolecule type: DNA A,Rolecule type: DNA A,Rolecule type: DNA A,Resperimental source: strain PCC 7120 C,Genetics: A,Gene: alr2308 Query Match B82.5%; Score 47; DB Best Local Similarity 77.8%; Pred: No. 5.4; Matches 7; Conservative 0; Mismatches Qy 1 CPRECESIC 9	.; Sasamoto, S.; Watanabe, A.; Iriguo
A, Title: Complete Genomic Sequence of the Filame A, Reference number: AB1807; MUID:21595285; PMID: A, Accession: AE2094 A, Status: preliminary A, Molecule type: DNA A, Robert Edwes: 1425 «KUR» A, Experimental source: strain PCC 7120 C, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: 7; Conservative 0; Mismatches Ouery Match Best Local Similarity 77.8*; Pred: No. 5.4; Matches 7; Conservative 0; Mismatches Oy ICPRECESIC 9	
A; Reterence number: Ablau; Mulb: 11595285; FMLD: A; Accession: AE2094 A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-425 «KUR» A; Experimental source: strain PCC 7120 C; Genetics: A; Greet: alr2308 Query Match Best Local Similarity 77.8%; Pred: No. 5.4; Matches 7; Conservative 0; Mismatches Qy I CPRECESIC 9	tous Nitrogen-fixing Cyanobacterium P
A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Rosidues: 1425 «KUR» A;Cross-references: UNIPROT:Q8YUN1; GB:BA000019; A;Experimental source: strain PCC 7120 C;Genetics: A;Genetics:	7.59640
A; Molecule type: DNA A; Residues: 1-425 < KUR> A; Residues: 1-425 < KUR> A; Cross-references: UNIPROT: QSYUNI; GB: BA000019; A; Experimental source: strain PCC 7120 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Coust Natch Best Local Similarity 77.8%; Pred: No. 5.4; Matches 7; Conservative 0; Mismatches QY   CPRECESIC 9	
A;Cross-references: UNIPROT: Q8YUN1; GB:BA000019; A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr2308 Query Match Best Local Similarity 77.8%; Pred: No. 5.4; Matches 7; Conservative 0; Mismatches Qy 1 CPRECESIC 9	
Experimental source: strain PCC Senetics: Jene: alr2308 Juery Match Sest Local Similarity 77.8%; Atches 7; Conservative 0   CPRECESIC 9	PIDN:BAB74007.1; PID:g17131400; GSPDE
Juery Match 82.5%; Duery Match 82.5%; Astt Local Similarity 77.8%; Astches 7; Conservative 0	
Duery Match 82.5%; Sest Local Similarity 77.8%; Aatches 7; Conservative C 1 CPRECESIC 9	
dest Local Similarity 77.8%; fatches 7; Conservative C 1 CPRECESIC 9	; Length 425;
	2; Indels 0; Gaps 0;
Db 112 CPRPCEKIC 120	

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Gaps

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R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A; Pitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUD:21311952; PMID:11418146
A; Accession: B89813
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-487 < KUR>
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:099WD0; GB:BA000018; PID:g13700363; PIDN:BAB41661.1; GSPDB:GA
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: F86916
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R; Davies, R.M.; Davies, R.M.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MuID:21128732; PMID:11234002
A;Accession: F86916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9CDD4; GB:AL450380; NID:g13092455; PIDN:CAC29570.1; GSPDB:GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: A38963; "D0076
R;Matsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
Pereber Dyn. 203, 212-222, 1995;
A;Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expressive number: A38963; MUID:95383734; PMID:7655083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F86916
NADH-dependent glutamate synthase small subunit gltD [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
C;Accession: F86916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: 9-day embryo
R;Matsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori,
submitted to JIPID, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Spēcies: Gallus gallus (chicken)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 04-Apr-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 66;
0; Mismatches 3
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Pred. No. 66;
0; Mismatches
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C;Superfamily: Glutamate synthase, small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: gltD
C;Superfamily: Glutamate synthase, small subunit
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A;Molecule type: mRNA
A;Residues: 1-835 <MAT>
A;Cross-references: DDBJ:D45365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 375952
C;Accession: 575952
C;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q9S2220; EMBL:AL109849; PIDN:CAB52860.1; GSPDB:GN00070; SCOED A,Experimental source: strain A3(2)
C,Genetics:
A,Gene: gltD; SCOEDB:SC3A3.03c
C,Superfamily: glutamate synthase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH-glutamate synthase small subunit gltD [imported] - Staphylococcus aureus (strain N3 C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004 C;Accession: B89813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q55456; EMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BAA1079
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable glutamate synthase small chain - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Os-Nov-1999 #text_change 09-Jul-2004 C; Accession: T34868 R; Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, August 1999 A; Reference number: Z21560 A; Accession: T34868 A; Statuus: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 57;
1; Mismatches 3; Indels
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Pred. No. 66;
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                                                Indels
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                                                    ;
       Pred. No. 31;
4; Mismatches
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   similarity 44.4%;
4; Conservative ;
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ilarity 55.6%;
Conservative
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                                                                                                                                                                 146 CPQQCQPVC 154
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                                                                                                                    1 CPRECESIC 9
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Matches 4; Conserv
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Matches 6: Conserv
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A;Status: nucleic ad
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Query Match

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NyAlternate names: UL45h protein
C;Species: Marek's disease virus
A;Note: host Gallus gallus (chicken)
C;Date: 30-Jun-1991 sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: B22818; JQ2207
R;Ihara, T.; Kato, A.; Ueda, S.; Ishihama, A.; Hirai, K.
Virus Genes 3, 127-140, 1989
A;Title: Comparison of the sequence of the secretory glycoprotein A (gA) gene between Mdi
A;Reference number: A22818; MUID:90142542; PMID:2559540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Marek's disease virus homologue
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A;Cross-references: UNIPROT:021563; EMBL:266498; PIDN:CAA91291.1; GSPDB:GN00020; CESP:M1:
A;Experimental source: clone M195
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein M195.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23802
R;Button, Jo
R;Button, do the EMBL Data Library, October 1995
Gaps
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A,Residues: 1-211 <YAN>
A,Residues: 1-211 <YAN>
A,Cross-references: GB:L10283; NID:g388703; PIDN:AAA03152.1; PID:g388710
A,Experimental source: strain GA
C,Superfamily: turkey herpesvirus 23.5K protein
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Pred. No. 74;
2; Mismatches 2; Indels
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  Indels
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A; Residues: 1-211 < IHA>
A; Residues: 1-211 < IHA>
A; Expandida: N: Yoshida, S.; Nazerian, K.; Lee, L.F.
J. Gen. Virol. 74, 1837-1845, 1993
A; Title: Nuclectide and predicted amino acid sequences of R; Reference number: JQ2199; MUID:93389438; PMID:8397281
A; Accession: JQ2207
  3;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 51;
1; Mismatches
  Mismatches
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A;Introns: 90/3; 162/3; 207/3; 270/2
C;Superfamily: gliadin
  7;
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Best Local Similarity 55.6%;
Matches 5; Conservative
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
  5; Conservative
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162 CPRTCSVVC 170
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                                                   1 CPRECESIC 9
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     Matches
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C;Species: Bombyx mori (silkworm)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 12-Jul-2004
C;Accession: 552093; S70920
B;Kotani, B; Yamakawa, M:; Iwamoto, S:; Tashiro, M.; Mori, H.; Sumida, M.; Matsubara, F
Biochim. Biophys. Acta 1260, 245-258, 1995
A;Title: Cloning and expression of the gene of hemocytin, an insect humoral lectin which
A;Reference number: S52093; MUID:95178544; PMID:7873598
A;Description: A new gene, nel, encoding a Mr 93K protein with EGF-like repeats is stron
A;Reference number: JP0076
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C;Species: Marek's disease virus
A;Note inost Gallus gallus (chicken)
C;Date: 30-Unn-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
C;Accession: JS0389
R;Ihara, T.; Katc, A.; Ueda, S.; Ishihama, A.; Hirai, K.
Virus Genes 3, 127-140, 1989
A;Title: Comparison of the sequence of the secretory glycoprotein A (gA) gene between A;Reference number: A22818; MUID:90142542; PMID:2559540
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                                                                                                                                                          A; Experimental source: 9-day embryo
F;273-333/Domain: von Willebrand factor type C repeat homology <VWC>
F;395-592/Region: EGF-like repeats
F;444-80/Domain: EGF homology <EGFl>
F;486-521/Domain: EGF homology <EGF>
F;586-521/Domain: EGF homology <EGF>
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KResidues: 1-1566,'S',1568-3133 <MOR>
A;Cross-references: EMBL:D29738; NID:g474967; PID:g664884
C;Superfamily: hemolectin/hemocytin
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51;
                                                                                                                                                                                                                                                                                                                                               70.2%; Score 40; DB 2; 55.6%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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A;Residues: 1-3133 <KOT>
A;Cross-references: UNIPROT:P98092; EMBL:D29738
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A;Residues: 1-211 <1HA>
C;Superfamily: turkey herpesvirus 23.5K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Mori, H. submitted to the EMBL Data Library, April 1994 A;Reference number: $70920 A;Accession: $70920
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Pred. No.
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55.6%;
                                                   A;Accession: JP0076
A;Molecule type: mRNA
A;Residues: 1-835 <MA2>
A;Cross-references: DBDJ:D45365
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 CCKECQSVC 334
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Best Local Similarity
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Search completed: November 16, 2004, 14:30:51
Job time : 11.1887 secs
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C;Superfamily: formate dehydrogenase
C;Keywords: oxidoreductase
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                                                 Query Match 66.7%;
Best Local Similarity 55.6%;
Matches 5; Conservative
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Matches 5; Conservative
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A;Molecule type: DNA
A;Residues: 1-708 <KUR>
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A;Reference number: 219781
A;Accession: T23660
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-372 <WIL>
A;Residues: 1-372 <WIL>
A;Experimental source: UNIPROT:017969; EMBL:281573; PIDN:CAB04624.1; GSPDB:GN00020; CSSP:MC
C;Genetics:
                                                           C;Accession: A54660
R;Hofmann, S.L.; Topham, M.; Haieh, C.L.; Francke, U.
Genomics 9, 656-669, 1991
A;Title: CDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and lc
A;Reference number: A54660; MUID:91244309; PMID:2037293
                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P23327; GB:M60052; NID:g183918; PIDN:AAA88071.1; PID:g183919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P16230; GB:J05080; NID:g165099; PIDN:AAA31279.1; PID:g165100 C;Keywords: calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cidate: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
CiAccession: A34373
RiHofmann, S.L.; Goldstein, J.L.; Orth, K.; Moomaw, C.R.; Slaughter, C.A.; Brown, M.S.
J. Biol. Chem. 264, 18083-18090, 1889
A;Title: Molecular cloning of a histidine-rich Ca(2+)-binding protein of sarcoplasmic A;Reference number: A34373; MUID:90036884; PMID:2808365
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T23680
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A34373
histidine-rich calcium-binding protein precursor - rabbit
histories: Oryctolagus cuniculus (domestic rabbit)
C;Species: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
                             Gaps
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Pred. No. 1.4e+02;
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histidine rich calcium binding protein - human
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A;Cross-references: GDB:126369; OMIM:142705
A;Map position: 19q13.3-19q13.3
C;Keywords: calcium binding
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55.6%;
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818 CPLVCETVC 826
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Matches 5; Conserv
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A;Molecule type: mRNA
A;Residues: 1-852 <HOF>
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A;Molecule type: mRNA
A;Residues: 1-699 <HOF>
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens; A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:Q8YGB6; GB:AE008917; PIDN:AAL52424.1; PID:g17983227; GSPDB:Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      formate dehydrogenase (EC 1.2.1.2) [imported] - Brucella melitensis (strain 16M)
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3407
                                                                                                                                                                                       Gaps
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                                                                                                                        Length 372;
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                                                                                                                     Score 38; DB 2; Length 37;
Pred. No. 1.1e+02;
1; Mismatches 3; Indels
A;Map position: 2
A;Introns: 17/3; 72/3; 181/3; 232/2; 258/3; 294/3; 336/1
C;Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 38; DB 2; I 55.6%; Pred. No. 1.7e+02;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model protein search, using 1 OM protein November 16, 2004, 14:09:48; Search time 176.642 Seconds (without alignments) 62.956 Million cell updates/sec Run on:

US-10-784-537-1

1 CYNLCIRECESICGADGACWTWCADGCSRSC 31 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum

seq length: 0 seq length: 200000000 88 Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

A\_Geneseq\_23Sep04:\* .: geneseqp1980s:\* :: geneseqp1990s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2001s:\* geneseqp2000s:\* geneseqp20028:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20048:\*

## SUMMARIES

	Description	Abg60450 Selective	Abr56862 Aminopept	Adp31258 Human sec	Adp31260 Human sec	Adp31259 Human sec	Adp31058 Human sec	Adp30639 Human sec	Adp30638 Human sec	Adp30636 Human sec	Adp30692 Human sec	Adp30720 Human sec	Adp30699 Human sec	Adp30701 Human sec	Adp30712 Human sec	Adp30722 Human sec	Adp30565 Human sec	σ.	Abj38280 pAMG21-RA	Adp30630 Human sec	Adp30633 Human sec	w	Adp30910 Human sec	Adp30911 Human sec	Adp30681 Human sec	9
SUPERMITES	QI	ABG60450	ABR56862	ADP31258	ADP31260	ADP31259	ADP31058	ADP30639	ADP30638	ADP30636	ADP30692	ADP30720	ADP30699	ADP30701	ADP30712	ADP30722	ADP30565	ADP30749	ABJ38280	ADP30630	ADP30633	ADP30606	ADP30910	ADP30911	ADP30681	ADP31356
	1 DB	S	9	_	œ	_	œ _	œ	œ	œ	œ _	80	80	80	89	80	æ	60	9	œ	œ	œ	80	80	80	ω.
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de	Query Match	100.0	100.0	36.9	36.9	36.9	36.1	35.9	35.9	35.9		35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.6	35.4	35.4	35.4	35.1	35.1	34.8	34.3
	Score	198	198	73	73	73	71.5	71	71	71	71	71	71	71	71	71	71	71	70.5	70	70	70	69.5	69.5	69	99
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Adp30560 Human sec Abr55376 A polypep Ad123896 Buthoid 8 Adp3145 Human sec Adp30869 Human sec Adp30869 Human sec Adp31690 Human sec Adp31329 Human sec Adp31329 Human sec Adp31350 Human sec Adp31350 Human sec Adp31354 Human sec Adp31359 Human sec Adp31359 Human sec Adp31359 Human sec	Adp31117 Human sec Adp31119 Human sec Adp31210 Human sec Adp31211 Human sec Abb71150 Drosophil Abb58064 Drosophil
ADP30560 ABR53376 ADP31445 ADP31445 ADP31215 ADP31699 ADP31690 ADP3133 ADP3133 ADP31136 ADP31594 ADP31594 ADP31596	ADP31117 ADP31119 ADP31210 ADP31211 ABB71150 ABB58064
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2124 611 5815 7111 2358 930 930 4423 10444 1222 2272 2552 3036	3585 8973 1227 1344 2858 3060
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## ALIGNMENTS

ABG60450 standard; peptide; 31 AA RESULT 1 ABG60450 

ABG60450;

(first entry) 30-JUL-2002 Selective targeting peptide #125.

Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; aradiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic; gene therapy

Synthetic.

WO200220769-A1.

14-MAR-2002.

07-SEP-2001; 2001WO-US027692.

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.

(TEXA ) UNIV TEXAS SYSTEM.

Pasqualini R;

Arap W,

WPI; 2002-415731/44.

Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular disease.

Claim 22; Page 108; 317pp; English.

The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with ischaemia, cancer, arthritis, diabetes, cardiovascular disease,

Gaps

; 0

Length 31; Indels

Matches

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100.0%; Score 198; DB 6;
100.0%; Pred. No. 8.6e-14;
ive 0; Mismatches 0;
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                                                          Conservative
                                Similarity
31; Conser
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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17-SEP-2002;
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29-AUG-2002;
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inflammation or macular degeneration. Furthermore, the peptide is useful for diagnosing the diseases cited above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60126-ABG60574 represent selective targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Targeting peptide, obesity, lipodystropathy, anorectic, antilipaemic, peptide therapy, gene therapy, infection; human immunodeficiency virus, HIV, placental delivery, teratogenic, placenta, adipose, pancreatic, beta-3 integrin, beta-5 integrin, spleen, aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                             Length 31;
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                                                                                                                                                                                                                                                        100.0%; Score 198; DB 5;
100.0%; Pred. No. 8.6e-14;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR56862 standard; peptide; 31 AA
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                                                                                                                                              peptides of the invention
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                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                      Sequence 31 AA;
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                                                                                                                                                                                                                                                                                           Local
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Sequence 31 AA;

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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
31
           31
CYNLCIRECESICGADGACWTWCADGCSRSC
           CYNLCIRECESICGADGACWTWCADGCSRSC
                                                                                Human secreted protein SEQ ID #2025
                                           ADP31258 standard; protein; 2808
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2002US-0411019P.
2002US-0411022P.
2002US-0411023P.
2002US-0411024P.
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2002US-0410949P.
2002US-0410953P.
2002US-0410957P.
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2002US-0410959P.
2002US-0410960P.
2002US-0410961P.
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2003US-0463700P
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2002US-0406608P.
2002US-0406611P.
2002US-0406612P.
2002US-0406616P.
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2002US-0406642P.
2002US-0406646P.
2002US-0406653P.
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2002US-040666FP.
2002US-0410946P.
2002US-0410947P.
2002US-0410948P.
2002US-0410953P.
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2002US-0410958P.
2002US-0410959P.
2002US-0410960P.
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2003US-0463708P.
2003US-0463716P.
2003US-0463732P.
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2002US-0411082P.
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2003US-0467201P.
2003US-0467203P.
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2003US-0471336P.
2003US-0472420P.
                                                               28-AUG-2003; 2003WO-US026780
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2003US-0486960P.
2003US-0493341P.
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                      WO2004035732-A2.
  Homo sapiens.
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08-AUG-2003;
                                          29-APR-2004
 diseases
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                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule for diagnosing, preventing or treating disessuch as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                   Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1974 CTTTCTGTCCCACGAGGACCTGC--GCTTCC 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3256; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein SEQ ID #2027.
                                                                                                                                                                                                                                                                               (FIVE-) FIVE PRIME THERAPEUTICS INC
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                    2003US - 0463732P . 2003US - 0467199P . 2003US - 0467201P . 2003US - 0467201P . 2003US - 0471336P . 2003US - 0471336P . 2003US - 0472430P . 2003US - 0472430P . 2003US - 0476699P .
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2003US-0485223P.
2003US-0485224P.
2003US-0485325P.
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2003US-0493370P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
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18-APR-2003; 2
18-APR-2003; 2
18-APR-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
19-MAY-2003; 2
19-MAY-2003; 2
22-MAY-2003; 2
22-MAY-2003; 2
09-UUN-2003; 2
                                                                                                                                                                       08-JUL-2003;
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Matches
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The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and
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19-MAY-2003;
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                                                                                                                         New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                        The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antifilammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                              Beaurang PA, Behrens D;
Haishan L, Linnemann T;
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                                                                                                                                                                                                                                                                                                            Match 36.9%; Score 73; DB 8; Length 4683; Local Similarity 45.2%; Pred. No. 65; es 14; Conservative 1; Mismatches 14; Indels
                                                                                  Zhang H;
                                                                                                                                                                                                                                                                                                                                                                       2049 CTTTCTGTCCCACGAGGACCTGC--GCTTCC 2077
                                                                                                                                                                                                                                                                                                                                                       1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                               Hestir K,
                                                                                                                                                                     Claim 1; SEQ ID NO 3258; 428pp; English.
                                                            Williams LT, Chu K, Lee E, Hestir K,
Halenbeck RF, Huang MM, Kothakota S,
Pierce K, Wang Y, Wong JGP, Wu G, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein SEQ ID #2026.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADP31259 standard; protein; 4848 AA
                                           (FIVE-) FIVE PRIME THERAPEUTICS INC
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2002US-0406588P
2002US-040661B
2002US-0406611P
2002US-0406612P
2002US-0406616P
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08-AUG-2003; 2003US-0493370P.
08-AUG-2003; 2003US-0493573P.
08-AUG-2003; 2003US-0493577P.
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2002US-0406579P.
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29-AUG-2002;
29-AUG-2002;
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29-AUG-2002;
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29-AUG-2002;
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New nucleic acid molecule for diagnosing, preventing or treating dise such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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2003US-0493370P.
2003US-0493573P.
                  2002US-0411032P.
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002US-0411024P
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02-MAY-2003; 2
19-MAY-2003; 2
19-MAY-2003; 2
22-MAY-2003; 2
09-JUN-2003; 2
09-JUN-2003; 2
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18-APR-2003; 2
18-APR-2003; 2
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ADP30639
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treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                                                                                Score 73; DB 8; Length 4848;
Pred. No. 67;
1; Mismatches 14; Indels
                                                                                                                                                                                                      2214 CTTTCTGTCCCACGAGGACCTGC--GCTTCC 2242
                                                                                                                                                                                   CYNLCIRECESICGADGACWTWCADGCSRSC 31
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2002US-040668P
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2002US-0406612P
2002US-0406612P
2002US-0406642P
2002US-0406642P
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2002US-0411032P.
2002US-0411035P.
2002US-0411037P.
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es 14; Conserv
                                                                                   Sequence 4848 AA;
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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29-AUG-2002;
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2002US-0411073P.
2002US-041101P.
2002US-041101P.
2003US-0463700P.
2003US-046370P.
2003US-0463716P.
2003US-0463732P.
2003US-0463732P.
2003US-0463732P.
2003US-0463732P.
2003US-0463732P.
2003US-0463733P.
2003US-0467230P.
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2003US-0493341P.
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2003US-0486891P.
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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
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                                                                                                                                                                                                                                                              New nucleic acid molecule for diagnosing, preventing or treating disesuch as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Haishan L, Linnemann T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.9%; Score 71; DB 8; Length 291; 57.9%; Pred. No. 9.6; cive 2; Mismatches 6; Indels
                                                                                                                                                                                                         Zhang H;
                                                                                                                                                                               Hestir K,
                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2637; 428pp; English
                                                                                                                                                                              Williams LT, Chu K, Lee E, Hestir K,
Halenbeck RF, Huang MM, Kothakota S,
Pierce K, Wang Y, Wong JGP, Wu G, 2
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2002US-0406585P.
2002US-0406588P.
2002US-0406608P.
2002US-0406611P.
            2003US-0485325P.
2003US-0486446P.
2003US-0486840P.
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2003US-0493341P.
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                                                                                                                                                                                                                                   WPI; 2004-348438/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 291 AA;
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
08-JUL-2003; 2
08-JUL-2003; 2
14-JUL-2003; 2
15-JUL-2003; 2
15-JUL-2003; 2
08-AUG-2003; 2
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08-AUG-2003; 2
08-AUG-2003; 2
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Matches
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                                                      Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
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2003US-0463716P.
2003US-0463732P.
2003US-0467199P.
                            Human secreted protein SEQ ID
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2002US-0406608P.
2002US-0406611P.
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2002US-0411111P.
2003US-0463700P.
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2003US-0467203P.
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2003US-0476609P.
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2003US-0485218P.
2003US-0485223P.
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2002US-0411045P.
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2002US-0411048P.
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(first entry)
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18-APR-2003;
02-MAY-2003;
                                                                                                Homo sapiens.
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29-AUG-2002;
29-AUG-2002;
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02-MAY-2003;
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17-SEP-2002;
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17-SEP-2002;
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29-AUG-2002;
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7-SEP-2002;
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 12-AUG-2004
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                                The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antifilammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, ganetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence available on WIPOWEB and is not in the specification.
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                                                                                                                                                                                        8; Length 291;
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                                                                                                                                                                                        Score 71; DB 8 Pred. No. 9.6; 2; Mismatches
            Claim 1; SEQ ID NO 2636; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein SEQ ID #1403
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2002US-0406579P.
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                                                                                                                                                                                         Query Match 35.9
Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                Sequence 291 AA
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29-AUG-2002;
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17-SEP-2002;
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L, Linnemann T;
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), Haishan L, 
Zhang H;
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Halenbeck RF, Huang MM, Kothakota S, 1
Pierce K, Wang Y, Wong JGP, Wu G, Zh.
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2003US-046370BP.
2003US-0463716P.
2003US-0463732P.
2003US-046719P.
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2003US-0486480P.
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2003US-0486960P.
2003US-0493341P.
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           29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
17-SEP-2002;
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02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
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2002US-0411023P 2002US-0411024P

17-SEP-2002;

08-AUG-2003;

08-AUG-2003

19-MAY-2003; 22-MAY-2003; 22-MAY-2003; 09-JUN-2003;

17-SEP-2002; 17-SEP-2002;

17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 7-SEP-2002;

7-SEP-2002;

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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                        Human secreted protein SEQ ID #1459
                          ADP30692 standard; protein; 659 AA.
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2002US-0411019P.
2002US-0411022P.
2002US-0411023P.
2002US-0411024P.
2002US-0411032P.
2002US-0411035P.
2002US-0411041P.
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2002US-0411046P.
2002US-0411048P.
2002US-0411052P.
2002US-0411055P.
2002US-0411012P.
2002US-041101P.
2002US-0411111P.
2003US-0463700P.
2003US-0463708P.
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2002US-0410960P.
2002US-0410961P.
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2003US-0467230P.
2003US-0471306P.
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2002US-0410946P.
2002US-0410947P.
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2002US-0406653P.
2002US-0406655P.
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                                                                             (first entry)
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29-AUG-2002;
29-AUG-2002;
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17-SEP-2002;
17-SEP-2002;
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17-SEP-2002;
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                                                    ADP30692;
RESULT 10
            ADP30692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, anticinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule for diagnosing, preventing or treating disesuch as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Linnemann T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hestir K, Beaurang PA,
thakota S, Haishan L, L.
, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2634; 428pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams LT, Chu K, Lee E, Hestir K,
Halenbeck RF, Huang MM, Kothakota S,
Pierce K, Wang Y, Wong JGP, Wu G, Z
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                        2002US-0411041P.
2002US-0411045P.
2002US-0411048P.
2002US-0411048P.
2002US-0411048P.
2002US-0411073P.
2002US-041101P.
2002US-041101P.
2002US-041101P.
2002US-041101P.
2002US-041101P.
2002US-041101P.
2002US-041101P.
2003US-0463716P.
2003US-0463716P.
2003US-0463716P.
2003US-0463716P.
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2003US-0463716P.
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18-APR-2003;
18-APR-2003;
02-MAY-2003;
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02-MAY-2003;
02-MAY-2003;
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19-MAY-2003;
22-MAY-2003;
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09-JUN-2003;
09-JUN-2003;
08-JUL-2003;
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8 셤

Query Match Best Loca Matches

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Beaurang PA, Behrens D;
Haishan L, Linnemann T;
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Huang MM, Kothakota S,
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                                                                                                                               2002US-0406655P.
2002US-0406666P.
2002US-0410946P.
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2003US-0471336P
2003US-0472420P
2003US-0476609P
2003US-0476609P
2003US-0476641P
2003US-0485213P
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2002US-0411052P.
2002US-0411055P.
2002US-0411073P.
2002US-0411101P.
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2003US-0467201P.
2003US-0467203P.
2003US-0467230P.
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2002US-0410957P.
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2003US-0463716P.
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29-AUG-2002;
217-SEP-2002;
117-SEP-2002;
117-SEP-2002;
117-SEP-2002;
117-SEP-2002;
117-SEP-2002;
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17-SEP-2002;
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                                                                                                                                                                                                                                                                                   New nucleic acid molecule for diagnosing, preventing or treating disesuch as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Haishan L, Linnemann T;
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                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2690; 428pp; English.
                                                                                                                                                                                                                      Chu K, Lee E, Hestir K,
Huang MM, Kothakota S,
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       22-MAY-2003; 2003US-0472420P.
22-MAY-2003; 2003US-0472430P.
92-JUN-2003; 2003US-0476609P.
09-JUN-2003; 2003US-0476641P.
08-JUL-2003; 2003US-0485213P.
08-JUL-2003; 2003US-0485223P.
08-JUL-2003; 2003US-048632EP.
14-JUL-2003; 2003US-0486446P.
15-JUL-2003; 2003US-0486481P.
15-JUL-2003; 2003US-0486891P.
15-JUL-2003; 2003US-0486891P.
15-JUL-2003; 2003US-0486891P.
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                                                                                                                               2003US-0486960P.
2003US-0493341P.
2003US-0493370P.
2003US-0493573P.
 2003US-0471336P
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tes 11; Conservative
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                                                                                                                                                     08-AUG-2003;
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Matches
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ADP30720
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Sequence 659 AA;
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                                 New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                  The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antichifammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence as along a number of in the specification.
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Zhang H
                                                                   Claim 1; SEQ ID NO 2718; 428pp; English.
Wu G,
                                                                                                                                                                                                                                                                                                                                       Human secreted protein SEQ ID #1466.
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2002US-0406611P.
2002US-0406612P.
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2002US-0406640P.
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2002US-0410948P.
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2002US-0410953P.
Wong JGP,
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2002US-0410946P.
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                 WPI; 2004-348438/32.
Pierce K, Wang Y,
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29-AUG-2002;
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                              17-SEP-2002;
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17-SEP-2002;
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8; Length 659;

35.9%; Score 71;

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02-MAY-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
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09-JUN-2003; 2
08-JUL-2003; 2
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08-JUL-2003; 2
08-JUL-2003; 2
14-JUL-2003; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP30712;
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            ö
                                                                                                                             Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
             Gaps
            ;
            Indels
            9
      ed. No. 19;
Mismatches
      Pred. No.
                                                                                                                 Human secreted protein SEQ ID #1468
                                                                        ADP30701 standard; protein; 659 AA
57.9%; Pre-
                          CGADGACWTWCADGCSRSC 31
                                 35 CGAGGCCCTGCAGGCTTTC 53
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2002US-0406640P.
2002US-0406642P.
2002US-0406646P.
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2002US-0406655P.
2002US-0410946P.
2002US-0410948P.
2002US-0410948P.
2002US-0410948P.
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2002US-0410959P.
2002US-0410959P.
2002US-0410959P.
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2002US-0410959P.
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2002US-0411041P.
2002US-0411041P.
2002US-0411048P.
2002US-0411048P.
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                                                                                                   12-AUG-2004 (first entry)
    Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                               WO2004035732-A2.
                                                                                                                                                                                                                           29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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29-AUG-2002;
29-AUG-2002;
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
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17-SEP-2002;
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diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antihflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immunos metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule for diagnosing, preventing or treating disesuch as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2699; 428pp; English
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2003US-0463732P.
2003US-0467199P.
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2003US-047130F.
2003US-047130F.
2003US-047130F.
2003US-047130F.
2003US-0472430P.
2003US-047669P.
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2003US-0493341P.
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2003US-0486891P.
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Best Local Similarity
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2002US-0406588P.
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2002US-0406611P.
2002US-0406612P.
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2002US-0406640P.
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15-JUL-2003; 2003US-0486960P.
08-AUG-2003; 2003US-0493331P.
08-AUG-2003; 2003US-0493370P.
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2002US-0410962P.
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17-SEP-2002;
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17-SEP-2002;
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                      29-APR-2004
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                                                                                                                                                    New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                   The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antichinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, ganetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                  Beaurang PA, Behrens D;
Haishan L, Linnemann T;
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                                                                                             Zhang
                                                                  Williams LT, Chu K, Lee B, Hestir K,
Halenbeck RF, Huang MM, Kothakota S, 1
Pierce K, Wang Y, Wong JGP, Wu G, Zh
                                                                                                                                                                                                           Claim 1; SEQ ID NO 2710; 428pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein SEQ ID #1489.
                                        (FIVE-) FIVE PRIME THERAPEUTICS INC.
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2002US-040658PP.
2002US-040660BP.
2002US-040661P.
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2002US-040661P.
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08-AUG-2003; 2003US-0493573P.
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Matches 11; Conserv
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29-AUG-2002;
17-SEP-2002;
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ADP30722
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(FIVE-) FIVE PRIME THERAPEUTICS INC.
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2002US-0410959P
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17-SEP-2002;
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18-APR-2003;
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18-APR-2003;
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02-MAY-2003;
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09-JUN-2003;
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17-SEP-2002;
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22-MAY-2003;
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Beaurang PA, Behrens D; Haishan L, Linnemann T; Zhang Williams LT, Chu K, Lee E, Hestir K, Halenbeck RF, Huang MM, Kothakota S, 1 Pierce K, Wang Y, Wong JGP, Wu G, Zh.

## WPI; 2004-348438/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.

# Claim 1; SEQ ID NO 2720; 428pp; English.

The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory,

ö immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification. Gaps ö 8; Length 659; 6; Indels / Match 35.9%; Score 71; DB Local Similarity 57.9%; Pred. No. 19; nes 11; Conservative 2; Mismatches Search completed: November 16, 2004, 14:24:18 Job time: 178.642 secs 13 CGADGACWTWCADGCSRSC 31 CGAGGCCCTGCAGGCTTTC 53 Sequence 659 AA Query Match Best Local Si Matches 11; 35 88888 ઠે g

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Sequence 25, Appli
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-086-436-30
US-09-252-991A-22358
US-09-548-372D-13
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US-08-662-485A-25
US-08-633-314-25
US-08-933-314-24
US-08-933-314-25
US-08-92-70-767-38435
US-09-270-767-38435
US-09-270-767-38435
US-09-270-767-38435
US-08-472-053-4
US-08-952-3834-4
US-08-952-3834-1
US-09-627-650B-5
US-09-627-650B-5
US-09-627-650B-5
US-09-627-650B-5
US-09-627-650B-7
US-09-627-650B-7
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US-09-627-650B-7
US-09-627-650B-7
US-09-627-650B-7
US-09-627-650B-7
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US-09-252-991A-18845
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1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Sequence 30, Sequence 2235 Sequence 13,

58.5

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Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 19249, A
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 48539, A
Sequence 48539, A
Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-451-472-6

1 US-08-451-472-6

1 Sequence 6. Application US/08451472

1 Patent No. 5770192

2 GENERAL INFORMATION:

    APPLICANT:

    TITLE OF INVENTION: BIOLOGICAL CONTROL ACENTS

    NUMBER OF SEQUENCES: 73

    CORRESPONDENCE ADDRESS:

    ADDRESSER: Mixon & Vanderhye PC

    STREET: 8th Floor, 1100 No. 5770192th Glebe Road

    CITY: Arlington
    STREET: 8th Floor, 1100 No. 5770192th Glebe Road

    CITY: Arlington
    STREET: 8th Floor, 1100 No. 5770192th Glebe Road

    CITY: Arlington
    STREET: 8th Floor, 1100 No. 5770192th Glebe Road

    CONDITY: USA

    CONDITY: USA

    CONDITY: USA

    CONDITY: USA

    CONTRY: USA

US-09-548-367D-13
US-09-551-853D-13
US-09-548-375D-13
US-09-548-373D-13
US-09-548-36F-13
US-09-52-991A-19249
US-09-627-658-7
US-09-627-658-3
US-09-627-658-3
US-09-627-658-3
US-09-627-658-3
US-09-627-658-3
US-09-627-658-3
US-09-637-658-3
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US-09-637-658-3
US-09-637-658-3
US-09-637-658-3
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US-09-270-767-48539
US-08-820-970-9
US-08-896-449A-2
US-09-132-652-2
US-09-886-900A-2
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Best Local Similarity 50.0
Matches 10; Conservative
   MOLECULE TYPE: peptide
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   TOPOLOGY:
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amino acid
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                                                                            APPLICANT: ATKINSON, RONALD K
APPLICANT: ATKINSON, MERLIN E.H.
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.8%; Score 67; DB 1; Length 61; 55.6%; Pred. No. 1.9;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION DATA:

FILLING DATE: 17-JULY-1996

APPLICATION NUMBER: US/08/256,933

FILLING DATE: 27-JULY-1994

APPLICATION NUMBER: W9/08/15108

FILLING DATE: 29-JAN-1993

APPLICATION NUMBER: AU PL0722

FILLING DATE: 31-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Shaw, Melissa A.

REGISTRATION NUMBER: 38,301

REGISTRATION NUMBER: PPD 5099/D1

TELEFRANCE/DOCKET NUMBER: PPD 5099/D1

TELEFRANCES 510-231-1122

INFORMATION FOR SEQ 1D NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   Sequence 25, Application US/08682485A Patent No. 5763568 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 3: Zeneca, Inc.
1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 CIRECESICGADGACWIW 22
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                                                                                                                                                                                                                                                                                     CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 10; Conserv
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ORGANISM: Le
                                                                                                                                                                                                                                                 ADDRESSEE:
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JS-08-682-485A-25
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Sequence 4, Application US/08451472 Patent No. 5770192 GENBRAL INFORMATION: APPLICANT:

RESULT 3 US-08-451-472-4

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Gaps
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Pred. No. 1.9;
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TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
WHWER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILIATION NUMBER: US/08/451,472
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816 4000
TELEFAX: (703) 816 4100
TELEFAX: (704) 8100
TELEFAX: (70
                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,125
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: peptide
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Sequence 38435, Application US/09270767

Requence 38435, Application US/09270767

Regence 10. 6703431

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 38435

LENGTH: 79
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Sequence 53652, Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Number: 0326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 53652
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-38435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 CESICGADG-----ACWIWCADGCSRSC 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Drosophila melanogaster
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ORGANISM: Drosophila melanogaster
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; Sequence 2, Application US/08472053
; Patent No. 6689356
; GENERAL INFORMATION:
21 CNKECKSYGGSYGYCWTW 38
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APPLICANT: MAEDA, SUSUMU
APPLICANT: MCCHCHEN, BILLY F.
APPLICANT: HAMMOCK, BRUCE D.
APPLICANT: FOWLER, ELIZABETH
APPLICANT: BELAGAJE, RAMA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Conservative
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Best Local Similarity
                                                                                                                 US-09-270-767-38435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAEDA, SUSUMU
APPLICANT: MACCUTCHEN, BILLY F.
APPLICANT: MACCUTCHEN, BILLY F.
APPLICANT: FOWLER, ELIZABETH
APPLICANT: FOWLER, ELIZABETH
APPLICANT: BELAGAJE, RAMA M.
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE OF INVENTION: 1082CT TOXINS
CURRENT APPLICATION NUMBER: US/08/472,053
CURRENT FILING DATE: 1994-04-15
PRIOR APPLICATION NUMBER: 07/629603
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1990-12-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENCY H. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Leiurus quinquestriatus quinquestriatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Leiurus quinquestriatus quinquestriatus
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Pred. No. 1.9;
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              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-UDX-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-UDX-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PLO722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: 38,301
TELECOMMUNICATION NUMBER: 38,301
TELECOMMUNICATION NUMBER: 38,301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08472053
; Patent No. 6689356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.8%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 amino acids
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Best Local Similarity 55.6'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
  CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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5 CIRECESICGADGACWTW 22

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US-08-952-383A-14
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TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE REPERENCE: UTOSB.1FWCDS.
CURRENT APPLICATION NUMBER: US/08/472,053
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 08/229417
PRIOR PLICATION NUMBER: 07/29603
PRIOR PILING DATE: 1994-04-15
PRIOR FILING DATE: 1994-04-15
PRIOR FILING DATE: 1994-12-19
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 61
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ZLOTKIN ELIAHU
APPLICANT: ZLOTKIN ELIAHU
APPLICANT: MAEDA, SUSSUM
APPLICANT: MACHA, BRILLY F.
APPLICANT: HAMMOCK, BRUCE D.
APPLICANT: FOWLER, ELIZABETH
APPLICANT: BELAGAL, ERONBINANT BACULOVIRUSES PRODUCING
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES
FILE REPERENCE: USOS: 1FWCE)
CURRENT APPLICATION NUMBER: US/08/472,053
CURRENT FILING DATE: 2002-11-13
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Pred. No. 3.9;
4; Mismatches
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PRIOR FILING DATE: 1994-04-15
PRIOR FILING DATE: 1994-04-15
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1980-12-19
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                          j ORGANISM: Leiurus quinquestriatus hebraeus
US-08-472-053-2
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US-08-472-053-46
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US-08-952-383A-14
; Sequence 14, Application US/08952383A
; Patent No. 6096304
; Patent No. Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, Application US/08472053
Patent No. 6689356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CIRECESICGADGACWIW 22
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.3%;
Best Local Similarity 50.0%;
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 9; Conservative
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APPLICANT: BILLY F. MCCUTCHEN
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT BACULOVIRUSES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY
TITLE OF INVENTION: RECOMBINANT BACULOVIRUS INSECTICIDES NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 3.5 INCH
COMPUTER: IBM
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD FOR WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 80;
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Pred. No. 4.9;
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,120
FILING DATE: DECEMBER 22, 1995
ATTOMEY/ABENT INFORMATION:
NAME: BEARDELL, LORI Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BA-9078
TELEPHONE: 302-992-4926
TELEFEHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BA-9078
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; Sequence 27, Application US/08970264A
; Patent No. 6322781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: FLOYD. LINDA AXAMETHY
REGISTRATION NUMBER: 33.692
REFERENCE/DOCKET NUMBER: BA-90
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 CIRECESICGADGACWTW 22
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.00
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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GENERAL INFORMATION:

APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematoode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
TITLE OF INVENTION: Methods Related Thereto
FILE REPERENCE: P-1095corrected
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-09
PRIOR PILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REPERBENCE: 21101.0009U3
CURRENT APPLICATION NUMBER: 08/09/627,650B
CURRENT APPLICATION NUMBER: 08/436,063
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 60/107,727
PRIOR PELING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
SEQ ID NOS: 50
                                                                                                                                                                                                                              Score 61.5; DB 3; Length 5405;
Pred. No. 3.5e+02;
4; Mismatches 10; Indels 3
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                                                                                                                                                                                                                                                                                                                        2 YNLCIRECESICGA-DG--ACWTWCADGC 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-436-063C-5; Sequence 5, Application US/09436063C; Patent No. 6407210
: LELEPAX: (703) 205-8000
: TELEPAX: (703) 205-8000
: INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 aminor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 41.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.74
Conservative
11, Conservative
                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                             amino acid
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US-09-627-650B-5
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                                                           Score 64; DB 3; Length 80; Pred. No. 4.9;
                                                                                                       5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08718388
Patent No. 6271362
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HARADA, MINORU
APPLICANT: HARADA, NAOKI
TITLE OP INVENTION: GENE ENCODING IGG FC REGION-BINDING
TITLE OP INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64; DB (
Pred. No. 5.2;
                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
FILE REPERENCE: BB1375 US NA
CURRENT APPLICATION INDMER: US/09/599, 632
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140,410
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WIRPHY JR., GERALD M
REGISTATION NUMBER: 28,971
REFERENCE/DOCKET NUMBER: 0230-111
                                                                                                                                                                                                                                                                                         Sequence 22, Application US/09599632
Patent No. 6768002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Leiurus quinquestriatus
US-09-599-632-22
                                                                                                                                              5 CIRECESICGADGACWIW 22
                                                                                                                                                                         40 CDKECKAYGGSYGYCWTW 57
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                                                             Query Match 32.3%;
Best Local Similarity 50.0%;
Matches 9; Conservative
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; MOLECULE TYPE: protein US-08-970-264A-27
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Best Local Similarity
Matches 9; Conserva
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Gaps

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Indels

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US-09-436-063C-5
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Query Match 30.6%; Score 60.5; DB 4; Length 1917; Best Local Similarity 40.7%; Pred. No. 1.8e+02; Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps g ò

Search completed: November 16, 2004, 14:32:10 Job time : 44.2013 secs

<u>.</u>;

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(without alignments)
75.615 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/BCD FNEW PUB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
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6: /cgn2 6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
8: /cgn2 6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
9: /cgn2 6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
10: /cgn2 6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
11: /cgn2 6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
12: /cgn2 6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
13: /cgn2 6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES		
Result No.	Score	Query	Query Match Length DB	DB	ΩI	Description	
-	198	100.0	31	16	US-10-363-204-125	Sequence 125, App	
7	71	35.9	3147	15	US-10-307-817-562	Sequence 562, App	
٣	71	35.9	3147	15	US-10-307-817-563	Sequence 563, App	
4	71	35.9	3288	14	US-10-184-644-477	Sequence 477, App	
ß	71	35.9	3288	14	US-10-184-634-477	Sequence 477, App	
9	70.5	35.6	7285	14	US-10-145-206-28	28, 7	
7	70	35.4	3233	14	US-10-123-155-81	81,	
80	70	35.4	3233	14	US-10-146-731-81	81,	
6	70	35.4	3233	14	US-10-140-472-81	81,	
10	70	35.4	3233	14	US-10-141-761-81	81,	
11	70	35.4	3233	14	US-10-142-885-81	81,	
12	70	35.4	3233	14	US-10-158-790-81	81,	
13	70	35.4	3233	14	US-10-137-871-81	Sequence 81, Appl	

Sequence 81, Appl Sequence 177, App Sequence 177, App Sequence 491, App Sequence 585, App Sequence 233, App Sequence 233	233,
US-10-140-923-81 US-10-141-756-81 US-10-141-759-81 US-10-140-864-81 US-10-140-864-81 US-10-142-426-81 US-10-142-426-81 US-10-143-136-177 US-10-146-731-491 US-10-146-731-491 US-10-146-731-491 US-10-141-761-491 US-10-141-761-491 US-10-140-923-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-141-756-491 US-10-142-426-491	0-146-731- 0-140-472- 0-141-761- 0-142-885- 0-158-790- 0-137-871- 0-140-923-
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### ALIGNMENTS

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Publication US/10363204
Publication No. US20040170955A1
GENERAL INFORMATION:
APPLICAMY:
APPLICAMY:
Board of Regents, The University of Texas System
APPLICAMY:
BOARD OF Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 125
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100.0%; Pred. No. 3.3e-14;
ative 0; Mismatches 0;
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JOCATION: (1)..(31)

COTHER INFORMATION: synthetic construct

US-10-363-204-125
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US-10-307-817-562
Sequence 562, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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nes 31; Conservative
US-10-363-204-125
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Best Local S:
Matches 31
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LENGTH: 3288
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
PLICATION DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REPERENCE: 21402-502C CURRENT APPLICATION NUMBER: US/10/307,817 CURRENT FILING DATE: 2002-12-02 NUMBER OF SEQ ID NOS: 682 SOFTWARE: CuraSeqList version 0.1 SEQ ID NO 562 LENGTH: 3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 563, Application US/10307817
Publication No. US20040058338A1
GENERAL INFORMATION:
APPLICANT: Age et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSeqList version 0.1
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Pred. No. 36;
2; Mismatches 14; Indels ::
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Pred. No. 36;
2; Mismatches 14; Indels
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Best Local Similarity 41.9%;
Matches 13; Conservative
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Best Local Similarity 41.9%;
Matches 13; Conservative
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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ORGANISM: Homo sapiens
US-10-307-817-562
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US-10-307-817-563
APPLICANT: Agee et al
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US-10-184-644-477
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LENGTH: 3147
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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                                                                                                                                               Score 71; DB 14; Length 3288; Pred. No. 37; 2; Mismatches 6; Indels
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                       35.9%;
il Similarity 57.9%;
11; Conservative
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SOFTWARE: Patentin version 3.1
SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO
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Godowski, Paul J.
Gurney, Austin L.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William I.
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Smith, Victoria
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ORGANISM: Homo Sapien
TYPE: DNA
ORGANISM: Homo Sapien
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Matches 11; Conserv
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US-10-184-644-477
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                                                                                                                                                       Query Match
Best Local
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APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: ACREA
APPLICANT: Shang, Zemin
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPREBNCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT PILING DATE: 2002-05-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 81
LENGTH: 3233
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
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Publication No. US20030138888A1
GENERAL INFORMATION:
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                           Stewart, Timothy A.
                                                                                                                                                                                     Tumas, Daniel
Watanabe, Colin K
Wood, William
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
                                                             Gurney, Austin L.
Sherwood, Steven
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Best Local Similarity 44.4*
Matches 12; Conservative
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Filvaroff, Ellen
                                                                                                                           Smith, Victoria
Goddard, Audrey
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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                                                          NAME/KEY: misc feature OTHER INFORMATION: Xaa (Posl,2,3,15,16,17) are each independently absent or amino oTHER INFORMATION: id residues;
OTHER INFORMATION: Xaa (Pos5,6,7,9,13) are each independently amino acid residues.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9330NG30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
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Best Local Similarity 40.0%; Pred. No. 78;
Matches 14; Conservative 1; Mismatches
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Pred. No. 47;
1; Mismatches
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OTHER INFORMATION: DAMG21-RANK-Fc vector
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Smith, Victoria
Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Deforge, Laura
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Gerritsen, Mary E
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Filvaroff, Ellen
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APPLICANT: Beredini, Mauree
APPLICANT: Beredini, Mauree
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Geriteen, Mary
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CORGANISM: Homo Sapien
US-10-123-155-81
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 3233
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CURRENT FILING DATE: 2002-05-10
                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
                                                                           LENGTH: 3233
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
PILE REFERENCE: P3330R1C248
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330410198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT PILING DATE: 2002-05-08
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                                                                       US-10-141-761-81
; Sequence 81, Application US/10141761
; Publication No. US20030148432A1
; GENERAL INFORMATION:
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Stewart, Timothy A.
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Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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APPLICANT: Beresini, Maureen
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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; ORGANISM: Homo Sapien
US-10-141-761-81
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LENGTH: 3233
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Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 81
LENGTH: 3233
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1; Mismatches
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Pred. No. 4
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Pred. No. 4
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                                                                                                                                                                                                                                                           5 CIRECESICGADGACWTWCADGCSRSC 31
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 81, Application US/10158790 Publication No. US20030180879A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Beresini, Maureen
APPLICANT: DeForger, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
                                                                                                                                                                         Query Match
Best Local Similarity 44.4%;
Matches 12; Conservative
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
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APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: WOOD SECOND OF SEC
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C188
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CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
ERQ ID NO 81
LENGTH: 3233
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Publication No. US20030207355A1
GENERAL INFORMATION:
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Gerritsen, Mary E.
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Wood, William
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                                             Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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; ORGANISM: Homo Sapien
US-10-137-871-81
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CORGANISM: Homo Sapien
US-10-140-923-81
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C200
CURRENY APPLICATION NUMBER: US/10/141,756
CURRENY TILING DATE: 2000-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 81
LENGTH: 3233
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                  Sequence 81, Application US/10141756
Publication No. US20030207359A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                          Stewart, Timothy A.
                                                                                                                               DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
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Gurney, Austin L.
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; ORGANISM: Homo Sapien
US-10-141-756-81
US-10-141-756-81
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APPLICANT:
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APPLICANT:
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Gaps

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; YYEE: PRI
ORGANISM: Artificial Sequence
; PEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(31)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    November 16, 2004, 14:19:17; Search time 505.943 Seconds (without alignments) 67.889 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
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                                                                                                                                                                                                       6730630 segs, 1107998698 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                     Title:
Perfect score:
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Maximum DB 8
                                                                                                                                              Sequence:
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SUMMARIES

Re	esult No.	Score	Query Match	Length	88	ΩI	Description
	п (	198	100.0	31	٦,	-27692A-	Sequence 125, App
	7 6	861	000	7 5		FCT-USUZ-2/836-58	Seguenc
	<b>1</b> 4	198	0.00	7 17		115-10-383-204-123	Segmence 123, App
	· LO	198	100.0	31		US-10-784-537-9	Sequence 9, Appli
	9	73	36.9	2808		PCT-US03-26780-3256	Sequence 3256, Ap
	7	73	36.9	4683		PCT-US03-26780-3258	Sequence 3258, Ap
	Φ (	73	36.9	4848		PCT-US03-26780-3257	Sequence 3257, Ap
	ν. <u>-</u>	, I.	36.4	707		PCT-USU3-26/80-3056 DCT-11803-26780-2634	Seguence 3036, Ap
	11	71	. o.	291		PCT-US03-26780-2634	Sequence 2636, Ap
	12	17	35.9	291		PCT-US03-26780-2637	Sequence 2637, Ap
	13	11	35.9	629		PCT-US03-26780-2690	Sequence 2690, Ap
	4. 1.	17	35.9	620		PCT-US03-26780-2697	Sequence 2697, Ap
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	12	1.17	35.9	629		PCT-US03-26780-2718	Sequence 2718, Ap
	18	7.1	35.9	629		PCT-US03-26780-2720	Sequence 2720, Ap
	19	11	35.9	1478		PCT-US03-26780-2563	Sequence 2563, Ap
	50	7.	35.9	2803		PCT-US03-26780-2747	Sequence 2747, Ap
	21	ני	35.9	3147		US-10-307-817-562	Sequence 562, App
	2 6	7.7		3198		US-10-307-817-383 US-60-592-191-182	Sequence 182. App
	24	17	35.9	3288		US-10-176-912-477	Sequence 477, App
	25	71	35.9	3288		US-10-179-524-477	Sequence 477, App
	56	17	35.9	3288		US-10-184-634-477	Sequence 477, App
	27	7 7	35.9	3288		US-10-184-644-477	Sequence 4//, App
	0 0	7.7	35.0	4725		US-00-592-191-190	Sequence 190. App
	308	1,1	35.9	4812		US-60-592-191-189	Sequence 189, App
	31	70.5	35.6	7285		PCT-US02-15273-28	Sequence 28, Appl
	32	70.5	35.6	7285		US-10-145-206-28	Sequence 28, Appl
	m c	70.5	35.6	7285		US-10-145-206A-28	Sequen
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	36	2,0	35.4	375		PCT-US03-26780-2604	equence
	37	70	35.4	3233		US-10-137-8,71-81	Sequence 81, Appl
	38	20	35.4	3233		US-10-158-790-81	Sequen
	93	9,	35.4	3399		PCT-US04-07434-47	Sequence 47, Appl
	\$ F	. מ ני	20°	1401		US-U/-629-603-/ TR-09-759-130B-177	Cauchien
	4 4	vo	7. 1.	1401	3 "	-790-177	Sequence 177. App
	4 4	<b>١</b> ٥	35.1	2700	, -	US03-26780-290	equence 2908,
	44	6	35.1	2700	-	3-2678	quence 2909,
	45	69	34.8	1475	56	.10-063-545-7	Sequence 79, A
						ALIGNMENTS	
2 2	RESULT 1	-276924.	-125				
ί	Sequen	ce 125, App	Applic		C/T	PC/TUS0127692A	
•	GENERA	GENERAL INFORMATION:	MATION:		٠	E 9	1
٠. ٠	TITLE	CANT: BO	BATA OF	Human	מעלים	Verbity of lexas Pargeting Pentide	system s Identified by Phage Display
٠.	FILE	REFEREN	CE: 005	774.P00	3 PCI		7
	CURRE	NT APPL:	ICATION	NUMBER	2	PCT/US01/27692A	
•	CURRE	CURRENT FILING DATE: 2001-09-07	NG DATE	2001	-09	0.7	
••	NOMBE	R OF SE(	D ID NO	S: 251			
٠.	SEO ID	NO 125	1117110	10101	;		
. ••	LENG	TH: 31					
••	TYPE	TYPE: PRT	1				

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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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APPLICANT: PASQUALINI
APPLICANT: PASGUALINI
TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: POR THE TREATMENT OF CANCER
FILE REPERENCE: UTSC: 872US
CURRENT FILING DATE: 2004-02-33
PRIOR FILING DATE: 2002-08-30
PRIOR PELLORINO NUMBER: PCT/USO1/27692
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR PELLORINO NUMBER: 60/231,266
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR FILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR FILING DATE: 2001-09-08
PRIOR FILING DATE: 2001-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PRIOR DATE: 2000-09-08
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Matches 31; Conservative 0; Mismatches
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                                                                                                        RESULT 4
US-10-784-537-1
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TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
TITLE OF INVENTION: and Adipose Tissues
FILE REFERENCE: 5774.P009PCT
CURRENT APPLICATION NUMBER: PCT/US02/27836
PRIOR APPLICATION NUMBER: PCT/US01/27692
PRIOR APPLICATION NUMBER: PCT/US01/27692
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 144
SEQ ID NO 58
LENGTH: 31
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APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America APPLICANT: only)
APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of
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                  100.0%; Score 198; DB 1; Length 31; 100.0%; Pred. No. 4.3e-14; tive 0; Mismatches 0; Indels
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                                                                                                        1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
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I.OCATION: (1)..(31);
OTHER INFORMATION: synthetic construct
US-10-363-204-125
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; Sequence 58, Application PC/TUS0227836
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               Query Match
Best Local Similarity 100.
Matches 31, Conservative
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FILE REFERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: PCT/US03/26780
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
TITLE OF INVENTION: THEIR USE
FILE REPERENCE: 08940.0014-00314-0031/26780
CURRENT APPLICATION NUMBER: PCT/US03/26780
CURRENT FILING DATE: 2003-08-28
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GENERAL INFORMATION:
APPLICANT: FIVERENE THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE
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PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PELICATION NUMBER: 60/406, 655
PRIOR APPLICATION NUMBER: 60/406, 642
PRIOR APPLICATION NUMBER: 60/406, 640
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406, 640
PRIOR APPLICATION NUMBER: 60/406, 588
PRIOR APPLICATION NUMBER: 60/406, 588
PRIOR APPLICATION NUMBER: 60/406, 588
PRIOR PILING DATE: 2002-08-29
PRIOR PLILING DATE: 2002-08-29
PRIOR PLILING DATE: 2002-08-29
PRIOR PLILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406, 666
PRIOR PILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406, 653
PRIOR PLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406, 653
PRIOR PLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406, 653
PRIOR PLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406, 653
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                                                              TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
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Best Local Similarity 100.0%; Pred. No. 4.3e-14;
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45.2%; Pred. No. 67;
Live 1; Mismatches
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Best Local Similarity 45.2<sup>†</sup>
Matches 14; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 2808
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SEQ ID NO 9
LENGTH: 31
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FRIOR PILING DATE: 2003-08-28
FRIOR APPLICATION NUMBER: 60/406,616
FRIOR FILING DATE: 2002-08-29
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FRIOR PILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
FRIOR APPLICATION NUMBER: 60/406,666
FRIOR APPLICATION NUMBER: 60/406,666
FRIOR FILING DATE: 2002-08-29
FRIOR PILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
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SEQ ID NOS: 3700
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PCT-US03-26780-2636
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Matches
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GENERAL INFORMATION:

TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THERE USE

FILE REFERENCE: 08940.0014-00304

CURRENT PELING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/406,616

PRIOR APPLICATION NUMBER: 60/406,655

PRIOR APPLICATION NUMBER: 60/406,655

PRIOR APPLICATION NUMBER: 60/406,640

PRIOR APPLICATION NUMBER: 60/406,640

PRIOR PILING DATE: 2002-08-29

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TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
TITLE OF INVENTION: THEIR USE
FILE REFERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: PCT/US03/26780
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Best Local Similarity 45.2%; Pred. No. 76;
Matches 14; Conservative 1; Mismatches
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SOFTWARE: Patentin version 3.2
SEQ ID NO 3257
LENGTH: 4848
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PCT-US03-26780-3056
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PCT-US03-26780-3257
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Best Local Similarity
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                                                                                                                     TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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PRIOR PLILING DATE: 2003-09-29
PRIOR PLILING DATE: 2002-08-29
PRIOR PAPLICATION NUMBER: 60/406,642
PRIOR PLILING DATE: 2002-08-29
PRIOR PLING DATE: 2002-08-29
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 2636
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see 11; Conserv
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PCT-US03-26780-2690
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SEQUENCE 2637, Application PC/TUS0326780

GENERAL INFORMATION:

APPLICANT: FYTERIME THERAPEUTICS, INC.

TITLE OF INVENTION: HUMAN POLYEPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYEPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE.

FILE REPERENCE: 08440.0014-00304

CURRENT APPLICATION NUMBER: PCT/US03/26780

CURRENT APPLICATION NUMBER: 60/406, 516

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/406, 655

PRIOR APPLICATION NUMBER: 60/406, 642

PRIOR PLING DATE: 2002-08-29

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                                                                                                                                                                                              35.9%; Score 71; DB 1; Length 291; 57.9%; Pred. No. 19; tive 2; Mismatches 6; Indels
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Best Local Similarity 57.99
Matches 11; Conservative
                                            TYPE: PRT; ORGANISM: Homo sapiens
PCT-US03-26780-2636
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PCT-US03-26780-2637
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LENGTH: 291
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FCT-USU3-26780-2697

Sequence 2897, Application PC/TUS0326780

GENERAL INFORMATION:

APPLICANT: FYTENERIME THERAPEUTICS, INC.

TITLE OF INVENTION: THEIR USE

CURRENT PILING DATE: 2003-08-28

PRIOR PELICATION NUMBER: 60/406,616

PRIOR PELICATION NUMBER: 60/406,616

PRIOR PELING DATE: 2002-08-29

RIOR FILING DATE: 2022-08-29
PRIOR PLILING DATE: 2002-08-29
PRIOR PLING DATE: 2002-08-29
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Matches 11; Conservative
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GENERAL INVORMATION:

**APPLICANT: FIVERRINE THERAPEUTICS, INC.**

**TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE

**FILE REPERENCE: 08940.0014-00304

**CURRENT APPLICATION NUMBER: PCT/US03/26780

**CURRENT PILING DATE: 2002-08-29

**PRIOR PILING DATE: 2002-08-29

**PRIOR PILING DATE: 2002-08-29

**PRIOR PAPLICATION NUMBER: 60/406,655

**PRIOR PAPLICATION NUMBER: 60/406,642

**PRIOR PILING DATE: 2002-08-29

**PRIOR APPLICATION NUMBER: 60/406,666

**PRIOR PILING DATE: 2002-08-29

**PRIOR PILING DATE: 2002-08-29

**PRIOR APPLICATION NUMBER: 60/406,666

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                                                                                                                     Query Match 35.9%; Score 71; DB 1; Length 659; Best Local Similarity 57.9%; Pred. No. 36; Matches 11; Conservative 2; Mismatches 6; Indels
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SEQ ID NO 2699
LENGTH: 659
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PCT-US03-26780-2699
; ORGANISM: Homo sapiens
PCT-US03-26780-2697
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Search completed: November 16, 2004, 14:46:42 Job time: 506.943 secs

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Sequence 48, Application US/10411910B
Sequence 48, Application US/10411910B
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
TITLE REFERENCE: H2041203-P
CURRENT APPLICATION NUMBER: US/10/411,910B
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 363
SOFTWARE: Patentin version 3.2
SEQ ID NO 48
ILENGTH: 844
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US-10-411-910B-48
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US-10-489-071-60
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Sequence 56, Appl
Sequence 58, Appl
Sequence 105, App
Sequence 23, Appl
Sequence 27, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 13625, A
Sequence 104, Appl
Sequence 29, Appl
Sequence 229, Appl
Sequence 229, Appl
Sequence 225, Appl
Sequence 225, Appl
Sequence 275, Appl
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9253, Ap
14189, A
14197, A
14188, A
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Sequence 1
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-411-910B-48

US-10-489-071-56

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US-10-976-102-52

US-10-976-102-33

US-10-846-989-57

US-10-846-989-57

US-10-873-923-13625

US-10-976-102-89

US-10-976-102-89

US-10-976-102-89

US-10-973-923-1365

US-10-10-101-72

US-10-220-366A-27561

US-10-220-366A-27561

US-10-220-366A-27561

US-10-220-366A-27561

US-10-734-949-13

US-10-732-923-9353

US-10-732-923-9353

US-10-732-923-14189

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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Sequence 60, Application US/10489071
GENERAL INFORMATION:
APPLICANT: PASQUALINE ET AL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OP USE OF TARGETING PEPTIDES AGAINST
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
FILE REFERENCE: UTSC:856US
CURRENT APPLICATION NUMBER: US/10/489,071
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SEQ ID NO 60
LENGTH: 13
LENGTH: 13
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                      Sequence 363, Apple Sequence 14218, A Sequence 14308, A Sequence 5576, Apple Sequence 5516, Apple Sequence 1204, Apple Sequence 1104, Apple Sequence 14190, A Sequence 14191, A Sequence 79, Apple 50, App
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5731, Ap
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97, Appl
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Sequence
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                                            US-10-732-923-14218

US-10-976-102-65

US-10-220-366A-14308

US-10-732-923-5576

US-10-732-923-5576

US-10-732-923-5545

US-10-732-923-1545

US-10-732-923-14190

US-10-732-923-14190

US-10-732-923-14190

US-10-976-102-78

US-10-976-102-79

US-10-976-103-833

US-10-980-888-97
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                                                                                                   ##PENLICANT: COGG, SCOCE |
### APPLICANT: COGG, SCOCE |
### TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS |
#### FILE REFERENCE: 00786/351004 |
### CURRENT APPLICATION NUMBER: US/09/205,658 |
### CURRENT FILING DATE: 2001-09-25 |
### PRIOR PELLING DATE: 1998-12-03 |
### PRIOR PELLING DATE: 1998-12-03 |
### PRIOR PELLING DATE: 1998-05-15 |
### PRIOR APPLICATION NUMBER: 08/885,34 |
### PRIOR APPLICATION NUMBER: US98/10080 |
### PRIOR PELLING DATE: 1999-05-15 |
### PRIOR PELLING DATE: 1999-05-15 |
### NUMBER OF SEQ ID NOS: 331 |
### SOFTWARE: FastSEQ for Windows Version 4.0 |
### ILENGTH: 383 |
### ILENGT
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Sequence 52, Application US/10976102

GENERAL INFORMATION:
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT APPLICATION NUMBER: 09/950,933
PRIOR APPLICATION NUMBER: 60/227

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

NUMBER: OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 383;
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Pred. No. 7.4;
2; Mismatches
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GENERAL INFORMATION:
APPLICANT: BODMEN, MARK WILLIAM
APPLICANT: BRIEND, EWANUEL CYRILLE PASCAL,
APPLICANT: CHAMPION, BRIAN ROBERT
                            Sequence 105, Application US/09963693B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-963-693B-105
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Best Local Similarity 46.2%;
Matches 6; Conservative 2
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Matches 7; Conservative
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                                                         GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
APPLICANT: Ogg, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-765-727-23
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SEQUENCE 56, Application US/10489071
GENERAL INFORMATION:
APPLICANT: PASQUALINE ET AL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
FILLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
FILLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
CURRENT APPLICATION NUMBER: US/10/489,071
CURRENT FILLING DATE: 2002-03-08
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SSOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 56
LENGTH: 9
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Sequence 58, Application US/10489071

Sequence 58, Application US/10489071

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST

TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES

TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES

TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES

CURRENT PELLING DATE: 2004-03-08

PRIOR FILING DATE: 2004-03-08

PRIOR FILING DATE: 2002-08-30

NUMBER OF SEQ ID NOS: 144

SEQ ID NO 58

LENGTH: 31
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                         Score 53; DB 6; Length 844;
Pred. No. 2.4;
2; Mismatches 4; Indels
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Pred. No. 7.4e+04;
0; Mismatches 1; Indels
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                            63.1%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                   177 CGRVCPHSCEAQC 189
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1 CYNLCIRECESIC 13
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Matches 8; Conservative
                                                                                         Conservative
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Query Match
Best Local Similarity
7; Conserve
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US-09-963-693B-105
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Application US/10883805
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HAPPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
CHER REFERENCE: 67452-2010
CURRENT APPLICATION NUMBER: US/10/765,727
CURRENT FILING DATE: 2004-01-23
FRIOR FILING DATE: 2002-07-25
FRIOR APPLICATION NUMBER: GB 0118153.6
FRIOR PILING DATE: 2001-07-25
FRIOR PILING DATE: 2001-07-25
FRIOR PELICATION NUMBER: GB 0207930.9
FRIOR APPLICATION NUMBER: GB 0212282.8
FRIOR APPLICATION NUMBER: GB 0212282.8
FRIOR PELING DATE: 2002-04-05
FRIOR FILING DATE: 2002-05-28
FRIOR PELING DATE: 2002-05-28
FRIOR APPLICATION NUMBER: GB 0212283.6
FRIOR FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 40
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Pred. No. 58;
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Pred. No. 58;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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TITLE OF INVENTION: MEDICAL TREATMENT
FILE REFERENCE: 654525-2012
CURRENT APPLICATION NUMBER: US/10/846,989
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/GB02/05133
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR PILING DATE: 2001-11-14
PRIOR FILING DATE: 2005-09-10
NUMBER OF SEQ ID NOS: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: RAGNO, SILVIA
APPLICANT: RAGNO, SILVIA
APPLICANT: TUGAL, TAMARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/10846989 GENERAL INFORMATION:
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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US-10-846-989-57
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LENGTH: 2471
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LENGTH: 2471
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RESULT 9 US-10-883-805-3

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GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)
CURRENT PILING DATE: 2003-12-10
PRIOR PLING DATE: 2003-12-10
PRIOR FILING DATE: 2002-12-04
NUMBER: OF SEQ ID NOS: 24149
SEQ ID NO 13625
LENGTH: 1363
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Pred. No. 4.3;
2; Mismatches
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Pred. No. 46;
0; Mismatches
GENERAL INFORMATION:
APPLICANT: INCTE PHARMACEUTICALS, INC.
APPLICANT: TAM, Y. Tom
APPLICANT: TAM, Preet:
APPLICANT: TAM, Preet:
APPLICANT: GUGLEY, Neil C.
APPLICANT: GUGLER, Karl J.
APPLICANT: GUGLER, Karl J.
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, Chandra
APPLICANT: PAUGHN, Mariah R.
APPLICANT: TUB, Henry
TITLE OF INVENTION: HUMAN EPIDERMAL PROTEINS
FILE REFERENCE: PF-0567 PCT
GURRENT APPLICATION NUMBER: US/106
PRIOR APPLICATION NUMBER: US/206, 817
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: US/206, 817
PRIOR FILING DATE: 1998-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte Clone No: 1798487
US-10-883-805-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.6%;
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US-10-732-923-13625
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPKVCPREC 9
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Sequence 72, Application US/10510101 GENERAL INFORMATION:
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 229
; LENGTH: 1370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
SEQ ID NO 72
LENGTH: 2768
                                                                                                                                                                 Query Match 52.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 CQKVCPTICKSH 226
                                                                                                                                                                                                                                                                                        215 COKVCPTICKSH 226
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Best Local Similarity 58.3
Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPARED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: US/09/963,693B
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: 08/886,534
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1999-05-15
                     APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Use
FILE REPERENCE: 1278D
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT FILING DATE: 2004-10-27
PRIOR APPLICATION NUMBER: 09/950,933
PRIOR FILING DATE: 2004-09-13
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.4%; Score 44; DB 5; Length 370; 58.3%; Pred. No. 18; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 6; Length 80;
Pred. No. 4.4;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 229, Application US/10482029; GENERAL INFORMATION:
APPLICANT: ODIN medical A/S
TITLE OF INVENTION: Oncology drug innovation
FILE REFERENCE: P 573 PC00
CURRENT APPLICATION NUMBER: US/10/482,029; CURRENT FILING DATE: 2003-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 331
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104, Application US/09963693B
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
        APPLICANT: Navarro Acevedo, Pedro A.
                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-10-976-102-89
                                                                                                                                                                                                                                                                                                                                                                                                  52.4%;
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-693B-104
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US-09-963-693B-104
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US-10-482-029-229
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LENGTH: 370
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Gaps
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APPLICANT: Clinton, Gail
APPLICANT: Roberts, Charles T
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING DISEASE
FILE REFERENCE: 49321-125
CURRENT APPLICATION NUMBER: US/60/616,596
CURRENT FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.2
SEQ ID NO 20
LENGTH: 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (734)...(734)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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APPLICANT: Eshioka, Glenn
APPLICANT: Shioka, Glenn
APPLICANT: Fishes, John
APPLICANT: Sette, Johnam
TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
FILE REFERENCE: 2060.009PC05
CURRENT APPLICATION NUMBER: US/10/510,101
CURRENT FILING DATE: 2004-10-05
PRIOR FILING DATE: 2002-09-26
PRIOR FILING DATE: 2002-09-26
PRIOR FILING DATE: 2002-09-05
PRIOR FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.4%; Score 44; DB 8; Length 1382; 58.3%; Pred. No. 63; 3; Indels cive 2; Mismatches 3; Indels
Score 44; DB 6; Length 1370;
Pred. No. 63;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                               RESULT 14
US-60-616-596-20
US-60-616-596-20, Application US/60616596
; GENERAL INFORMATION:
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; LOCATION: (1028)..(1028)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: (2501)..(2501)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-510-101-72
                                                                                                                                                                                                                                                                                    Query Match 52.4%; Score 44; DB 6; Length 2768; Best Local Similarity 77.8%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 2; Indels
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0; Gaps

Search completed: November 16, 2004, 14:47:13 Job time : 6.88679 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 16, 2004, 14:15:03; Search time 14.717 Seconds (without alignments) 84.991 Million cell updates/sec Run on:

US-10-784-537-3 84

1 CPKVCPRECESNC 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		مبق			SUMMARIES	
Result No.	Score	Query Match	, Length	DB	ΙD	Description
-	54	64.3	1363	7	T43220	insulin-like growt
7		63.1	425	~	AE2094	cal
٣	52	61.9		~	JE0142	8
4		60.7	4	~	H72230	
S		59.5		П	XKPOT	O)
9		59.5		~	G95318	FdxB ferredoxin II
7		59.5		~	JE0352	mucin MUCSB, trach
80	20	59.5	1513	~	T23681	hypothetical prote
σ	49	58.3		~	A70477	8
10	49	58.3		~	A46602	glutamate synthase
11	49	58.3		N	D87696	
12	48	57.1		~	B41132	collagen-related p
13	47	56.0		-	FERF3C	ferredoxin 2[4Fe-4
14	47	56.0		N	H85852	probable oxidoredu
15	47	56.0		~	A64983	hypothetical prote
16	47	56.0		7	F91008	probable oxidoredu
17	47	56.0		~	S57245	insulin receptor (
18	47	56.0	7	Н	A56081	insulin receptor -
19	46	54.8		~	T08072	proteinase inhibit
20	46	54.8		~	T09288	late embryonic abu
21	46	54.8	388	~	T31887	hypothetical prote
22	46	54.8		~	T31888	
23	46	54.8	395	7	S75952	_
24	46	54.8		~	T31889	_
25	46	54.8		~	T31898	hypothetical prote
56	46	54.8		N	JC4335	ro
27	45	53.6		N	T16735	hypothetical prote
28	45	53.6	4	N	$\sim$	glutamate synthase
29	45	53.6	472	N	G85985	glutamate synthase

glutamate synthase	glutamate synthase	glutamate synthase	glutamate synthase	NADH-glutamate syn	glutamate synthase	probable oxidoredu	hypothetical prote	proteinase inhibit	proteinase inhibit	trypsin inhibitor-	probable gibberell	proteinase inhibit	proteinase inhibit	proteinase inhibit	glutamate synthase
AB0907	D91140	G65112	AG0432	B89813	H82523	AF0042	T20561	T07597	TIEO1	JQ2269	A84713	S24973	S43105	JQ2153	E86785
~	~	~	~	~	~	7	~	N	-	~	~	~	~	N	7
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472	47	47	47	48	49	67	728	158	25	53	103	147	154	397	47
								53.0 156							•
									52.4	52.4					•

## ALIGNMENTS

insulin-like growth factor-1 receptor - common lancelet N;Alternate names: insulin-like peptide receptor C;Species: Branchiostoma lanceolatum (common lancelet) C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

Claces in 1920 wedge medical control of the control

Gaps ö Length 1363; 5; Indels Score 54; DB 2; Pred. No. 8.6; 0; Mismatches Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative (

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1 CPKVCPRECESNC 13 ઠે

206 cokvepescharc 218 g

hypothetical protein alr2308 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004
C;Accession: AE2094
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Attle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2094
A;Status: preliminary
A;Residues: preliminary
A;Residues: AE304
A;Residues: AE304
A;Residues: AE305
A;Accession: AE205
A;Accession: AE205
A;Accession: AE206
A;Accession:

A;Cross-references: UNIPROT:Q8YUN1; GB:BA000019; PIDN:BAB74007.1; PID:g17131400; GSPDB:G1 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: a1r2308

Gaps ö Query Match 63.1%; Score 53; DB 2; Length 425; Best Local Similarity 61.5%; Pred. No. 5.1; Matches 8; Conservative 0; Mismatches 5; Indels

Gaps

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Biochemistry 21, 752-756, 1982
A;Title: Primary structures of two low molecular weight proteinase inhibitors from potatc
A;Reference number: A90465; WUID:82182863; PMID:7074039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: G95318
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse, falman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot: A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:0922X89; GB:ABD006469; PIDN:AAK65113.1; PID:g14523551; GSPDB:GI A;Experimental source: strain 1021, megaplasmid pSymb R;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A:; Abola, P:; Ampe, F:; Barloy-Hubler, pela, D:; Chain, P:; Cowie, A:; Davis, R.W.; Dreano, S:; Federspiel, N.A.; Fisher, R.F.; L:; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.G. A;Reference number: Asolo39; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CjAccession: JE0352
R;Offner, G.D.; Nunes, D.P.; Keates, A.C.; Afdhal, N.H.; Troxler, R.F.
Biochem. Biophys. Res. Commun. 251, 350-355, 1998
A;Title: The amino-terminal sequence Of WUCSB contains conserved multifunctional D domai.
A;Reference number: JE0352; MUID:99009274; PMID:9790959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: pyruvate synthase subunit porD; ferredoxin 2{4Fe-4S} homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Species: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PdxB ferredoxin III [imported] - Sinorhizobium meliloti (strain 1021) magap.
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                          A, Accession: A01318
A, Modecule type: protein
A, Mesidues: 1-51 cHas>
A, Cross-references: UNIPROT: P01079
A, Cross-references: UNIPROT: P01079
C, Superfamily: potato proteinase inhibitor PTI
C, Keywords: serine proteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 105;
                                                                                                                                                                                                                                                                                 51;
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                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 50; DB 2; 50.0%; Pred. No. 4.8; ive 5; Mismatches
                                                                                                                                                                                                                                                                                      DB 1
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                      Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mucin MUC5B, tracheobronchial - human
                                                                                                                                                                                                                                                                                      59.5%;
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CPKVCPRECESN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                         33 PNVCPRNCDTN 43
                                                                                                                                                                                                                                                                                                                                                                                         2 PKVCPRECESN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :||||:|:::
CARVCPRDCQTH
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A; Residues: 1-1321 <OFF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: G95318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: fdxB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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C;Species: Thermotoga maritima
C;Species: In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: H72230
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
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A;Cross-references: UNIPROT:Q9X1X5; GB:AE001806; GB:AE000512; NID:g4982196; PIDN:AAD3670
A;Experimental source: strain MSB8
                                                                                                                                                                                                        Glutamate synthase (EC 1.4.1.-) small chain - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Accession: JE0142
R;Lu, T.; Wu, Y.Q.; Song, H.Y.
A;Taile: The nucleotide sequence of gltD gene encoding the small subunit of Rhodobacter
A;Reference number: JE0142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H72230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:008340
A,Note: the authors translated the codon CTG for residue 24 as Lys,CAC for residue 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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C;Species: Solanum tuberosum (potato)
C;Baccies: Solanum tuberosum (potato)
C;Baccesion: A01118
R;Hass, G.M.; Hermodson, M.A.; Ryan, C.A.; Gentry, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
6.8;
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Pred. No. 10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52; DB;
Pred. No. 6.8;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: TM1640
C;Superfamily: glutamate synthase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: gltD
C;Superfamily: glutamate synthase small chain
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.08;
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Best Local Similarity 60.00,
Best A 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 ČGRIČPODŘKČEGŇČ 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CPKVCP--RECESNC 13
                                                                                108 CPSDCPRPCEKIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.3.
Best Local 8; Conservative
                             CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-413 <LUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JE0142
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Gaps

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(EC 1.4.1.13) beta chain [validated] - Azospirillum brasilens
                                                                                                 C;Species: Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Accession: A46602; S10765; S51164
C;Accession: A46602; S10765; S51164
R;Pelanda, R.; Vanoni, M.A.; Perego, M.; Piubelli, L.; Galizzi, A.; Curti, B.; Zanetti, R;Pelanda, R.; Vanoni, M.A.; Perego, M.; Piubelli, L.; Galizzi, A.; Curti, B.; Zanetti, A;Biol. Chem. 268, 3099-3106, 1993
A;Title: Glutamate synthase genes of the diazotroph Azospirillum brasilense. Cloning, se A;Reference number: A46602; MUID:93155143; PMID:8428988
                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q05756; GB:L04300; NID:g289243; PIDN:AAA22178.1; PID:g304130 A;Experimental source: strain Sp7, strain ATCC 29145 and strain Sp6 A;Note: sequence extracted from NCBI backbone (NCBIN:124365, NCBIP:124371) R;Vanoni, M.A.; Negri, A.; Zanetti, G.; Ronchi, S.; Curti, B. Biochim. Biophys. Acta 10.99, 374-377, 1990 A;Title: Structural studies on the subunits of glutamate synthase from Azospirillum bras A;Reference number: S10764; MUID:90335272; PMID:2198943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Molecule type: protein
A; Residues: 2-19, X', 21-24; 328-332, A', 334-336, X', 338, X', 340, 'X', 342, 'X' < VANI>
R; Vanoni, M.A.; Mazzoni, A.; Fumagalli, P.; Negri, A.; Zanetti, G.; Curti, B.
Eur. J. Biochem. 226, 505-515, 1994
A; Title: Interdomain loops and conformational changes of glutamate synthase as detected
A; Reference number: S51033; MUID:95094808; PMID:8001567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glutamate synthase, small subunit [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
C;Accession: D8766-0
C;Accession: D876-0
C;Accession: D876-0
C;Accession: D876-0
C;Bethym, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; WUID:21173698; PMID:11259647
A;Accession: D87696
A;Scatus: prellminary
A;Molecule type: DNA
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: catalyzes the NAD(P)H-dependent reductive transfer of L-glutamine amide & Suberfamily: Glutamate synthase, small subunit C;Keywords: 3Fe-4S; iron-sulfur protein; metalloprotein; NADP; oxidoreductase F;48,51,56,60,95,99,105,109/Binding site: iron-sulfur clusters (Cys) (covalent) #status
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%; Score 49; DB 2; 46.7%; Pred. No. 19; ative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 2;
Pred. No. 19;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: CC3606
C,Superfamily: Glutamate synthase, small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGRICPODRLCEGNC 109
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Best Local Similarity 46.77
Best Local 7; Conservative
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A, Residues: 2-8;475-481 < VAN2>
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA; protein A; Residues: 1-481 <PEL>
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                                                                              glutamate synthase (NADPH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S10765
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A;Cross-references: GB:AF086604; NID:g3789926; PIDN:AAC67545.1; PID:g3789927
C;Comment: This protein is large multimeric glycoproteins which is secreted by epithelia
C;Genetics:
A;Gene: MUC5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamate synthase small subunit gltD - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Aug-2004
C;Accession: A70477
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
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A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: 281573; PIDN: CAB04625.1; GSPDB: GN00020; CESP: MQ
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Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.
                                                                                                                                                                                                                               Gaps
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A;Gene: CESP:M02G9.1
A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
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                                                                                                                                                                59.5%; Score 50; DB 2; Length 1321; 47.1%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 2; Length 1513;
Pred. No. 31;
1; Mismatches 5; Indels
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A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1513 <WILb
A;Cross-references: UNIPROT:017970; EMBL:Z81573; PII
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Pred. No. 19;
3; Mismatches
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C;Superfamily: Glutamate synthase, small subunit
                                                                                                                                                                                                                               2; Mismatches
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321 CPELCPRTCINMQHQNC 337
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Similarity 53.3%;
8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-476 < AQF>
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Best Local Similarity
Matches 8; Conserv
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probable oxidoreductase 23401 [imported] - Escherichia coli (strain 0157:H7,
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Best Local Similarity 53.3%;
Matches 8; Conservative
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C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 08-Dec-1999 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: B32308; A46701
R;Moreno-Vivian, C:; Hennecke, S.; Puehler, A.; Klipp, W.
J. Bacteriol: 171, 2591-2598, 1989
J. Hitle: Open reading frame 5 (ORF5), encoding a ferredoxinlike protein, and nifQ are cc
A;Reference number: A32308; MUID:89213944; PMID:2708314
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A; Mosicule type: DNA

A; Residues: 1-102 <MOR.

A; Residues: 1-102 <MOR.

A; Cross-references: UNIPROT: P20624; GB: M26323; NID: G341472; PIDN: AAA26146.1; PID: G516637

B; Jouanneau, Y.; Meyer, C.; Gaillard, J.; Forest, E.; Gagnon, J.

B; Biol. Chem. 268, 10636-10644, 1993

A; Title: Purification and characterization of a novel dimeric ferredoxin (FdIII) from Rh

A; Reference number: A46701; MUID: 93252956; PMID: 8387524
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                                                                                                            RESULT 12
B41132
collagen-related protein 2 - Hydra magnipapillata (fragment)
C;Species: Hydra magnipapillata
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 15-Sep-2003
C;Accession: B41132, S21991
B;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.
J. Cell Biol. 115, 1159-1169, 1991
A;Title: Mini-collagens in hydra nematocytes.
A;Reference number: A41132, MUID:92064646; PMID:1955459
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A;Molecule type: mRNA
A;Residues: 1-142 «KUR>
A;Cross-references: EMBL:X61046; NID:g9448; PIDN:CAA43380.1; PID:g9449
A;Note: submitted to the EMBL Data Library, July 1991
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Pred. No. 12;
4; Mismatches 2; Indels
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Pred. No. 11;
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A;Note: sequence extracted from NCBI backbone (NCBIP:131349)
C;Complex: homodimer
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46.2%;
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94 CGRICPQDRLCEGNC 108
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Matches 6; Conserv
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RESULT 14 , H85852

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A:Actual Heart_Canange Oy-Jul-2004

A:Accession: H86852

A:Actual Heart Columnation Heart 
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A,Residues: 1.412 <STO>
A)Cross-references: UNDROT:08X645; GB:AE005174; NID:g12516463; PIDN:AAG57284.1; GSPDB:GR
A,Experimental source: strain 0157:H7, substrain EDL933
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R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 77, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
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A;Molecule type: DNA
A;Residues: 1-412 <BLAPT
A;Cross-treferences: UNIPROT:P76440; GB:AE000303; GB:U00096; NID:g1788456; PIDN:AAC75207...
A;Experimental source: strain K-12, substrain M01655
C;Superfamily: Glutamate synthase, small subunit
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C,Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 16-Aug-2004
Species: Bscherichia coli
Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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Pred. No. 31;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: Z3401
C;Superfamily: glutamate synthase small chain
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caulobacter

Q9a2f9

Q9rn12 zymomonas m Q9hau2 homo sapien Q724f5 homo sapien Q9h7g8 homo sapien Q00485 hydra sp. m Q9h2g4 homo sapien Q744k2 synchococc Q8tjj7 methanosarc Q748c7 geobacter s Aar36449 geobacter Q6h27 rhodopseudo Cae26122 rhodopseu

09A2F9 09RNL2 09HAU2 02HAG8 00HAG8 00HAG2 09H2Q4 07HKZ 
Q8uw84 paralichthy

ALIGNMENTS

Q8UW84

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[1]
SEQUENCE FROM N.A.
STRAIN=17XNL;
                                                                                                                                                                                                                                      PubMed=12368865;
Query Match
                                                                                                                                                     Q7RMI4;
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Matches
                                                                                                                                 RESULT 1
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Q8rc72 thermoanaer
Q8rbw5 thermoanaer
Q7mbg7 wolinella s
Q74fu5 geobacter
Aar33841 geobacter
Q7uzu5 prohloroco
                                                                                                                                                                                                                                                                                                                                                                                    Q8gli4 synechococc
Qwcd4 porphyromon
Q9x1x5 thermotoga
Q89zr6 bacteroides
Q78547 neurospora
P01079 solanum tub
Q92zk9 rhizobium m
Q84156 solanum phu
Aas01731 solanum ph
O17970 caenorhabdi
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073kg0 treponema d
Aas12687 treponema
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                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                             November 16, 2004, 14:14:16; Search time 77.5094 Seconds (without alignments) 96.503 Million cell updates/sec
                                                                                                                                                                                                                                                                                Description
                                                                                                                                       1825181
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                         1825181 seqs, 575374646 residues
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ILPR BRALA
Q8YUN1
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©93KQ0
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©7MX5
Q92XX5
Q9 92K6
075547
Q92ZK9
Q92ZK9
Q94L56
AAS01731
MUSB HUWAN
Q8CAYS
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Maximum Match 100%
Listing first 45 summaries
                                 OM protein - protein search, using sw model
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QBRBW5
Q7MBG7
Q74FU5
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Q7UZU5
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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84
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Match Length DB
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Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                           Carlton J.W., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallm S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 419:512-519(zvuz).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                                                                                                                              Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 1359 AA; 158879 MW; FDBBC1141CCD176A CRC64;
                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
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PRT; 1359 AA
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01-07T-2003 (TrEMBLrel. 25, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last anno
Fe-S cluster containing protein.
Name=hyoB, OrderedLocusNames=Pro1714;
                                                  Created)
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                                          01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
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  PRELIMINARY;
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Q8P230 O67845 GLTD\_AZOBR

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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Insulin-like peptide receptor precursor (EC 2.7.1.112) (ILP receptor).
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Eukaryota, Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                             Wolf Y.I., Hess W.R.;
"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome.";
Proc. Natl. Acad. Sci. U.S.A. 100:1020-10025(2003).
EMBL; AE017166; AAQ00758.1; --
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0005108; P:electron transport; IEA.
InterPro; IPR001450; 4Fe4S_ferredoxin.
Ffam; PF00077; Fe44; 1.
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MEDLINE=96408719; PubMed=8813726;
Pashmforoush M., Chan S.J., Steiner D.F.;
"Structure and expression of the insulin-like peptide receptor from
                                                                                                                                                              Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
              Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Iron, Iron-sulfur, Metal-binding.
E 331 AA; 36610 MW; C5719BCDC5EFA817 CRC64;
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66.7%; Pred. No. 4.2;
ive 1; Mismatches 3; Indels
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                                                                                                  SEQUENCE FROM N.A.
STRAIN-SARG / CCMP 1375 / SS120;
MEDLINE-22810154; PubMed=12917486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PKVCPRECESNC 13
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    Prochlorococcus marinus.
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                                                                NCBI_TaxID=1219;
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002466;
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Insulin-like peptide receptor alpha chain
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Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 3.
Fibronectin type-III 4.
Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
Proton acceptor (By similarity).
                                                                                                                                                                                                                                                                                                                                   SMART; SM0060; FW3; 3.
SMART; SM00261; FU; 1.
SMART; SM00261; FU; 1.
PROSITE; PSC00853; FN3; 4.
PROSITE; PSC00107; PROTEIN KINASE ATP; 1.
PROSITE; PSC00109; PROTEIN KINASE DOM; 1.
PROSITE; PSC00109; PROTEIN KINASE TVR, 1.
PROSITE; PSC00239; RECEPTOR TYR KIN II; 1.
ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insulin-like peptide receptor beta chain
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Pred. No. 16;
0; Mismatches
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                                                                                                                                 InterPro; IRR006212; Furin repeat.
InterPro; IRR00930; Grow fac recept.
InterPro; IRR010030; Grow fac recept.
InterPro; IRR010109; Kinase.
InterPro; IRR010119; Prot Kinase.
InterPro; IRR01011; RecepttyrkinsII.
InterPro; IRR010145; Tyr pkinase.
InterPro; IRR010145; Tyr pkinase.
InterPro; IRR010145; Tyr pkinase.
Fam; PR001641; fin3; 3.
Ffam; PR00167; Furin-like; 1.
Ffam; PR00169; Fkinase; 1.
Ffam; PR010109; Recep L domain; 2.
PRINTS; PR00109; TYRXINASE.
PRODORO; PROF L MARINASE.
PRODORO; PROF L MARINASE.
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or send an email to license@isb-sib.ch)
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                              EMBL; S83394; AAB50848.1; -.
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InterPro; IPR003961;
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InterPro; IPR006212;
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Chen Y., Xue Y., Lai X., Huang L., Dong W., Yang J.,
Chen Y., Xue Y., Lai X., Huang L., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Mang J., Yu J., Yang H.;
Tan H., Chen R., Hang J., Yu J., Yang H.;
Chen Y., And J., Yu J., Yang H.;
The A complete sequence of the T. tengcongensis genome.";
Chenome Res. 12:689-700(2002)
Chenome Res. 12:680-700(2002)
Chenome Res. 12:68
                      GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0005118; P:electron transport; IEA.
GO; GO:0005118; P:electron transport; IEA.
InterPro; IPR001759; Adridx_reductase.
InterPro; IPR001037; FAD pyr_redox.
InterPro; IPR001037; FAD pyr_redox.
InterPro; IPR001031; Halical_ferredxn.
InterPro; IPR00001; Halical_ferredxn.
InterPro; IPR000205; NAD ES.
InterPro; IPR000103; Pyridine_redox_2.
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00070; Pyr redox; 1.
PRINTS; PR00353; 4FE4SFRDOXIN.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00469; PADPIN.
PRINTS; PR00469; PNDRDTASEII.
TIGRFAMS; TIGR01316; GltA; 1.
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ses 9; Conserv
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HSSP; Q28943; 1GTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 464 AA;
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Best Local Similarity
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Matches
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MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of the T. tengcongensis genome.";
Genome Res. 12:689-700 (2002).
EMBL; AE013026; AAM23842.1; -.
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MEDLINE-21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
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PRINTS; PROOJSS; 4FE4SFRDOXIN,
PROSITE; PSOO198; 4FE4S, FERREDOXIN; 1.
4FE-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SEQUENCE 425 AA; 46348 MW; 7237DCE3EFD6912E CRC64;
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Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
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Pred. No. 7.5;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Air2308 protein.
OrderedLocusNames=alr2308;
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
NADPH-dependent glutamate synthase beta chain and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO: GO:0005489; F:electron transporter activity; IEA. GO: GO:0005506; F:iron ion binding; IEA. GO: GO:006618; F:electron transport; IEA. IDEA. IDEA. DIACFPC: IPRO01450; Fe145_ferredoxin.
                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                            PRT;
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Local Similarity 61.5%;
Les 8; Conservative
                                          206 COKVCPESCLGNC 218
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1 CPKVCPRECESNC 13
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Query Match

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RESULT 5 Q8RC72

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EMBL; AE017208; AAR33841.1; -. TIGR; GSU0510; -.
                                                                                                               Science 302:1967-1969(2003).
EMBL; AE017180; AAR33841.1; -.
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Pubmed=14671304;
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les 7; Conserv
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                                                                                              environments."
                                                                                                                                                                 TIGR; GSU0510;
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X MEDLINE=22882897; PubMed=14500908;
A Mandarumar R., Gross R., Radatz G., Simon J., Lanz C., Klimmek O.,
Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
A Nandakumar R., Gross R., Radsta B.,
A Meyer F., Lederer H., Schuster S.C.;
"Complete genome sequence and analysis of Wolinella succinogenes.";
"REMBL, BX571658; CAE08617.1; -.
RO; GO:0015036; Pidsulfide oxidoreductase activity; IEA.
GO; GO:0015036; Pidsulfide oxidoreductase activity; IEA.
RO; GO:0015018; Pielectron transport; IEA.
RITEPPO; IPR001327; Abn Dyr reductase.
RITEPPO; IPR001137; Pyridine_redox.
RITEPPO; IPR0001037; Pyridine_redox.
RITEPPO; Pr0001037; Pyridine_redox.
RITEPPO; Pr0001037; Pyridine_redox.
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STRAID=DRA / ATCC 51573;
PubMeds-14671304; DOI=10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Medupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
                                                                                                                                                                                                                                                                                                                                                                                                        Wolinella succinogenes.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Wolinella.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Fe(III) reductase, beta subunit.
Name=sfrB; ORFNames=GSU0510;
Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
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  5;
                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATEDEHYDROGENASE (EC
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Pred. No. 11;
1; Mismatches 4; Indels
  Indels
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PRINTS; PR00368; FADPUR.
PRINTS; PR00469; PUDDDIASEII.
COMDLETE PROLEOME, OXIGOREGUCEABE.
SEQUENCE 649 AA; 72557 MW; CCAIE7589E36650D CRC64;
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  Mismatches
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Name=FDHB; OrderedLocusNames=WS0477;
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Local Similarity 61.5%;
hes 8; Conservative
                                                                                              90 CGRVCPQETQCERNC 104
                                                 1 CPKVCPRE--CESNC 13
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  9; Conservative
                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=844;
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Q7MBG7
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Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J., Khouri H.M., Peldblyum T.V., Utterback T.R., Man Aken S.B., Lovley D.R., Frager C.M.;
Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M., "Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
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InterPro; IRR00127; FAD_pyr_redox.
InterPro; IPR001037; FAD_pyr_redox.
InterPro; IPR00103; Pyridine_redox_2.
InterPro; IPR001100; Pyr_redox_1.
InterPro; IPR001100; Pyr_redox, 1.
InterPro; IPR00119; ADRNDRSE.
IRINTS; PR00419; ADRNDRSE.
IRINTS; PR00411; PNDRDTRASEI.
IRINTS; PR00491; PNDRDTRASEI.
IRINTS; PR00491; PNDRDTRASEI.
IRINTS; PR00491; PNDRDTRASEII.
IRINTS; PR00469; PNDRDTRASEII.
IRINTS; PR00469; PNDRDTRASEII.
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PROSITE; PS00119; PAZ ASP; UNKNOWN 1.
SEQUENCE 631 AA; 66824 MW; 55BAE2PC65C34C17 CRC64;
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Best Local Similarity 61...
8; Conservative
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                                                                                                              Query Match 61.9
Best Local Similarity 53.8
Matches 7; Conservative
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AAS12687;
                                             SEQUENCE
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Q73KQ0;
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MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

MADLINE N. Arellano A., Coleman M., Hauser L., Regala W., Shah M., Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M., Mebb E.A., Zinser E.R., Chisholm S.W.;

Mebb E.A., Zinser E.R., Chisholm S.W.;

Mebb E.A., Zinser E.R., Chisholm S.W.;

Mebb E.A., Zinser E.R., Chisholm S.W.;

Mebb E.A., Zinser E.R., Chisholm S.W.;

Nature 424:104-1047(2003).

Metal-1047(200596); Filon ion binding; IEA.

Metal-Pro; IPRO01450; 4Fe44. Ferredoxin.

Metal-Pro; IPRO01450; 4Fe44. FERREDOXIN; I.

Metal-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-0CT-2000 (TrEWBLrel. 15, Last sequence update)
01-MAR-2004 (TrEWBLrel. 26, Last amnotation update)
01-MAR-2004 (TrEWBLrel. 26, Last amnotation update)
01-MAR-2004 (TrewBlance) Streated abundant protein.
Arabidopsis thaliana (Mouse-ear cress)
Bukaryota, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                      Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S., Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB025624; BAB02467.1; -.
GO; GO:0005199; F:structural constituent of cell wall, IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 AA; 37282 MW; CBC53CA6F8A27AB3 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PMM1560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR011061; Antihaemostatic.
InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR009646; Root_cap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20277480; PubMed=10819329;
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PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 CPSNCPRPCERIC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 61.5
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=59919;
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AC 091774
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DT 01-0C
DT 01-MC
DT 01-MC
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                                                             Gaps
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STRAIN=ATCC 35405 / DSM 14222;

SUBMACH=1504399 DOI=10.1073/pnas.0307639101;

Submach=1504399 DOI=10.1073/pnas.0307639101;

Submach=1504399 DOI=10.1073/pnas.0307639101;

Dodson R.J., Davidsen T.M., Tettelin H., Eisen J.A., Heidelberg J.F.,

Selengut J., Ren Q., Brinkac L.M., Madupu R.F., Kolonay J.F.,

Selengut J., Ren Q., Brinkac L.M., Madupu R.F., Kolonay J.F.,

Gebregeorgis B., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,

Shateman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,

Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,

Weinstcock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;

"Comparison of the genome of the oral pathogen Treponema denticola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAY-2004 (TrEMBLrel. 27, Last annotation update)
04-MAY-2004 (TrEMBLrel. 27)
04-MAY-2004 (TremBlrel. 27)
                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Pyridine nucleotide-disulphide oxidoreductase family protein.
OrderedLocusNames=TDE2167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteome; Iron; Iron-sulfur; Metal-binding.
Length 631;
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                                                          4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with other spirochete genomes.";
Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
EMBL; AE017253; AAS12687.1; -.
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3
Score 52; DB 2
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                     914 AA.
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InterPro; IPR00159; Adradx reductase.
InterPro; IPR001327; FAD pyr_redox.
InterPro; IPR001037; FAD pyr_redox.
InterPro; IPR001031; Pyridine_redox_2.
Pfam; PF00070; Pgr4; 2.
Pfam; PF00070; Pyr_redox; 1.
PRINTS; PR00193; 4FE4SFRDOXIN.
PRINTS; PR00419; ADXRDFASE.
PRINTS; PR00419; PNDRDTASEII.
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Pred. No.
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4Fe-4S; Complete proteome; Iron: Iron-
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O7MTD4
RESULT 15
Q7MTD4
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                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 35405 / DSM 14222;

SURAIN=ATCC 35405 / DSM 14222;

Submed=15064399;

Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,

Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J., Durkin S.A.,

Daugherty S.C., Shetty J., Shvartsbeyn A., Gebregeorgis E., Geer K.,

Tsegaye G., Malek J.A., Ayodeji B., Shatsman S., McLeod M.P.,

Smajs D., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z.,

Xiang Q., Sodergren E., Baca E., Weinstock G.M., Norris S.J.,

Trang Q., Sodergren E., Baca E., Weinstock G.M., Norris S.J.,

"Comparison of the genome of the oral pathogen Treponema denticola

with other spirochete genomes.";

Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

R FIGR; TDE2167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PCC 7942;

MEDLINE-22450571; PubMed=12562813;

Matayama M., Kondo T., Xiong J., Golden S.S.;

"IdpA encodes an iron-sulfur protein involved in light-dependent modulation of the circadian period in the cyanobacterium Synechococcus elongatus PCC 7942.";

J. Bacteriol. 185:1415-1422 (2003).

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:000556; F:iron ion binding; IEA.

GO; GO:0005118; P:electron transport; IEA.

InterPro; IPR001450; 4Fe45; Erredoxin.

PEAM; PF00037; PET4; 1...
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              Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                    Score 52; DB 2; Length 914; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 2; Length 352;
Pred. No. 12;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                             914 AA; 101880 MW; 22E32CA9726D4FBE CRC64;
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PROSITE; PS00198; 4FE4S FERREDOXIN; 1.
4Fe-45; Iron; Iron-sulfur; Metal-binding.
SEQUENCE 352 AA; 37865 WW; 33614612158F2936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.7%;
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61.5%;
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Best Local Similarity 61.5.,
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                415 CGHVCPRYCEOGC 427
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                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                               Local Similarity
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                                       NCBI_TaxID=158;
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                        Query Match
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QBGLI4;
                                                                                                                                                                                                                                                                                                                                Matches
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CPIDCPRPCERVC 109

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Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J., Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.E., Fraser C.M., Galvin J.L., Duncan M.J., Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.", J. Bacteriol. 185:5591-5601(2003).

FMBL, AR017179, AAG66999.1;
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                                                                                                                                                                      Name=gltD; OrderediccusNames=PG2033;
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0015036; F:disulfide oxidoreductase activity; IEA. GO; GO:0005118; P:electron transport; IEA. InterPro; IPR000759; Adrndx reductase.
InterPro; IPR000759; Adrndx reductase.
InterPro; IPR0060137; FAD pyr. redox.
InterPro; IPR006004; Glut synth NADFH.
InterPro; IPR00103; Pyridine redox_2.
InterPro; IPR001100; Pyr. redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glutamate synthase, small subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO1316; gltA; 1.
PROSITE; PS00564; PFKB_KINASES_2; UNKNOWN_1.
Complete proteome.
SEQUENCE 462 AA; 49811 MW; 66B2E434EFE7A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 51; DB 60.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                                                                                  Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00070; Pyr redox; 1. PRINTS; PR00419; ADXRDTASE. PRINTS; PR004119; PADPNR. PRINTS; PR00411; PUDRDTASEI. PRINTS; PR00469; PUDRDTASEII
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   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=W83;
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